

APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: NOVEL MORPHOGEN-RESPONSIVE SIGNAL
TITLE OF INVENTION: TRANSDUCER AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,118
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VITO PHD, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: CRP-121 [2054/91]
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 905...1264
US-08-727-118-1

Query Match 74.0%; Score 14.8; DB 2; Length 3611;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGAGTGGCT 20
DB 3313 AGTTATGGAGAGTGGTT 3296

RESULT 44
US-08-774-528-235/C
Sequence 235, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619a1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441

SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 235
LENGTH: 3669
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (401)..(2806)
US-09-774-528-235
Query Match 74.0%; Score 14.8; DB 4; Length 3669;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGAGTGGCT 20
DB 1110 AGTTATGGAGAGAGGCT 1093

RESULT 45
US-08-162-809-17
Sequence 17, Application US/08162809
Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4049 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 10...2994
US-08-162-809-17

Query Match 74.0%; Score 14.8; DB 1; Length 4049;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGAGTGGCT 20
DB 2135 AGTTATGGAGAGTGGCT 2152

RESULT 46

US-08-162-809-11
; Sequence 11, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydoon G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4097 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..3042
US-08-162-809-11

Query Match 74.0%; Score 14.8; DB 1; Length 4097;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGAGTGGCT 20
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Db 2183 AGTTCATGGAGAGTGGCT 2200

RESULT 47
US-08-895-652A-1
; Sequence 1, Application US/09895652A
; Patent No. 6774223
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberta
; APPLICANT: Pillai, Rageswari
; TITLE OF INVENTION: Method of diagnosing, Monitoring, Staging, Imaging and
; TITLE OF INVENTION: Treating Colon Cancer
; FILE REFERENCE: DEX-0211
; CURRENT APPLICATION NUMBER: US/09/895,652A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,515
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4698
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (3921)
US-09-895-652A-1
Query Match 74.0%; Score 14.8; DB 4; Length 4698;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 AGTTAATGGAGAGTGGCT 20
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Db 2109 AGTTCATGGAGAGTGGCT 2126
RESULT 48
US-09-262-537-48
; Sequence 48, Application US/09262537
; Patent No. 6479256
; GENERAL INFORMATION:
; APPLICANT: Havlick, Joel
; TITLE OF INVENTION: Lectomedin Materials and Methods
; FILE REFERENCE: 27866/35307
; CURRENT APPLICATION NUMBER: US/09/262,537
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: 60/076,782
; EARLIER FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 5749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-262-537-48

Query Match 74.0%; Score 14.8; DB 4; Length 5749;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGC 19
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Db 1922 CAGTTGATGGAGAGTGGC 1939

RESULT 49
US-09-103-330-35
; Sequence 35, Application US/09103330A
; Patent No. 6319716
; GENERAL INFORMATION:
; APPLICANT: TIKOO, SURESH K.
; APPLICANT: BABLUK, LORNE A.
; APPLICANT: REDDY, POLICE S.
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
; FILE REFERENCE: 293102002121
; CURRENT APPLICATION NUMBER: US/09/103,330A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/880,234
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: 08/164,292
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 34446
; TYPE: DNA
; ORGANISM: Bovine adenovirus type 3
US-09-103-330-35

Query Match 74.0%; Score 14.8; DB 3; Length 34446;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGG 18
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Db 8536 GCAGATAATTGAGAGTGG 8553

RESULT 50
US-08-375-709-1/c
; Sequence 1, Application US/08375709
; Patent No. 5683898
; GENERAL INFORMATION:
; APPLICANT: YAZAWA, Kazunaga
; APPLICANT: YAMADA, Akiko
; APPLICANT: KATO, Seishi
; APPLICANT: KONDO, Kiyosi
; TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
; TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
; TITLE OF INVENTION: Eicosapentaenoic Acid
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,709
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,251
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-147945
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/150/A00K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37895 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Shewanella putrefaciens SCRC-2874 (PERM
; ORGANISM: BP-1625)
; US-08-375-709-1

Query Match 74.0%; Score 14.8; DB 1; Length 37895;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTTAATGGAGATGGCT 20
|||||
Db 377 AGTTAATGGCGAGTTGCT 360

Search completed: December 3, 2004, 05:52:51
Job time : 104.316 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 01:41:45 ; Search time 2536.05 Seconds
(without alignments)
287.374 Million cell updates/sec

Title: US-10-050-189A-8

Perfect score: 20
Sequence: 1 gcagttaatggagtggtgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hcc.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	187	7	CN633741 taf55b05.
C 2	17.4	87.0	338	7	CN771770 tad94d307.
C 3	17.4	87.0	357	7	CN772025 tad94d307.
C 4	17.4	87.0	381	7	CN634000 taf55b05.
C 5	17.4	87.0	427	2	BE102024
C 6	17.4	87.0	435	7	CN772716 tae06d02.
C 7	17.4	87.0	436	1	A1178866 EST222548
C 8	17.4	87.0	462	6	CB736658 AMGNNUC:M
C 9	17.4	87.0	517	7	CN553187 tae25e12.
C 10	17.4	87.0	540	7	CN777863 taf71806.
C 11	17.4	87.0	550	2	AW526046 UI-R-B01-
C 12	17.4	87.0	557	6	CB613159 AMGNNUC:N
C 13	17.4	87.0	593	2	BF563085 UI-R-B01-
C 14	17.4	87.0	673	4	BJ578386 BJ578386
C 15	17.4	87.0	705	4	BJ577489 BJ577489
C 16	17.4	87.0	740	4	BJ572384 BJ572384
C 17	17.4	87.0	744	4	BJ572099 BJ572099
C 18	17.4	87.0	746	5	BQ204219 UI-R-DN1-
C 19	17.4	87.0	754	6	CF283555 AGENCOURT
C 20	17.4	87.0	757	4	BJ570457 BJ570457
C 21	17.4	87.0	775	4	BJ570485 BJ570485
C 22	17.4	87.0	1091	7	CK163790 FGAS01642
C 23	17.4	87.0	1462	9	AG612934 Mus muscu
C 24	17.4	87.0	3276	3	AY325247 Rattus no

645	8	BZ224094	BZ224094
654	9	AG169335	AG169335 Pan trogl
683	8	BZ164877	BZ164877 CH230-246
729	9	BX169283	BX169283 Danilo ter
808	9	BX169508	BX169508 Danilo ter
812	6	CB684683	CB684683 OSJNEfl4H
828	2	AW080408	AW080408 xes3a08.x
249	7	CN210935	CN210935 Rt_Fcd_00
333	2	BF410784	BF410784 UI-R-CNO-
339	2	BE841809	BE841809 MRL1-SN006
344	7	CR477607	CR477607 CR477607
361	2	BF849242	BF849242 CM3-EN007
372	2	BF521948	BF521948 UI-R-YO-a
374	1	AI954046	AI954046 wx78n12.x
379	7	H37761	H37761 yp4cc03.s1
390	2	BF542969	BF542969 UI-R-YO-a
393	7	N33486	N33486 Yy42f09.s1
410	1	AI559323	AI559323 tq43f08.x
413	7	W42606	W42606 zc23d08.s1
415	2	BE349791	BE349791 hq43b08.x
417	7	R55760	R55760 Yg99c07.s1
418	7	CN388155	CN388155 170005313
431	7	CK100560	CK100560 C050P42.5
432	1	AA350346	AA350346 EST57669
440	1	AA436245	AA436245 zv24g02.s
442	1	AA648528	AA648528 ns22x06.s
447	7	H99886	H99886 Yx37h05.s1
457	6	CD539657	CD539657 B0215B07-
461	2	AW217984	AW217984 EST296699
465	1	AI170417	AI170417 EST216344
467	2	BF284013	BF284013 EST448604
467	2	AW917901	AW917901 EST349305
467	2	AW917902	AW917902 EST349206
471	2	AW192606	AW192606 x147e06.x
473	4	BI289988	BI289988 UI-R-DK0-
478	6	CD542571	CD542571 B0242A05-
485	1	AI716560	AI716560 UI-R-YO-a
494	4	BM818065	BM818065 K-EST0084
522	2	AW389529	AW389529 CM4-ST016
535	2	BE567119	BE567119 601341289
536	7	CO644824	CO644824 ILLUMIGN
547	2	BE294519	BE294519 601173467
548	8	AZ017711	AZ017711 RPCI-23-2
549	6	CD542400	CD542400 B0240A11-
550	4	BI303830	BI303830 UI-R-DSO-
553	8	AQ036740	AQ036740 CIT-HSP-2
554	4	BI291703	BI291703 UI-R-DMO-
557	1	AI819173	AI819173 wj32c06.x
559	7	N26041	N26041 Yx89c06.s1
566	1	AV772871	AV772871 AV772871
568	2	BE296626	BE296626 601173652
577	2	BF929375	BF929375 MRL1-HN006
597	6	CB147584	CB147584 K-EST0203
628	9	CR081886	CR081886 Forward S
630	7	CN208822	CN208822 Tor9329 G
638	8	AZ643717	AZ643717 IM0507016
644	9	CR176890	CR176890 Forward s
653	2	BE513527	BE513527 601315037
656	2	BE546469	BE546469 601077643
656	4	BG260626	BG260626 602371373
673	7	CN388144	CN388144 170005322
679	2	BE542056	BE542056 601066965
683	6	CA440796	CA440796 UI-H-DT1-
688	2	AW957365	AW957365 EST369555
691	6	CB155728	CB155728 K-EST0214
694	6	CB455808	CB455808 712984 MA
700	9	CE014089	CE014089 tigr-gss-
721	1	AL040597	AL040597 DKFp434K
730	9	BX976571	BX976571 Forward s
733	7	CN388149	CN388149 170004245
739	6	CA447139	CA447139 UI-H-EIO-
740	5	BQ060620	BQ060620 UI-H-EII-

c 98	16.8	84.0	745	9	AG489390	Mus muscu	171	16.4	82.0	1039	2	BE512735	BE512735	601171425
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101	16.8	84.0	776	7	CN388163	170005327	c 174	16.4	82.0	4105	3	BC058083	BC058083	Mus muscu
102	16.8	84.0	828	6	CD653621	AGENCOURT	c 175	16.4	82.0	4149	3	AK049286	AK049286	Mus muscu
103	16.8	84.0	840	5	BQ440033	AGENCOURT	c 176	16	80.0	190	6	CD022921	CD022921	NXPV 094
104	16.8	84.0	841	5	BQ434013	AGENCOURT	c 177	16	80.0	190	7	H73098	H73098	Y225h05.sl-
105	16.8	84.0	850	6	CD244035	AGENCOURT	c 178	16	80.0	213	7	T34979	T34979	EST518781
106	16.8	84.0	870	7	CF552181	AGENCOURT	c 179	16	80.0	251	7	Z40827	Z40827	HSC2GF012 n
107	16.8	84.0	876	6	CD105568	AGENCOURT	c 180	16	80.0	363	4	B1177836	B1177836	EST518781
108	16.8	84.0	887	4	BM449720	AGENCOURT	c 181	16	80.0	400	7	CO355973	CO355973	DR ATE.NR
109	16.8	84.0	913	2	B2303842	601868830	c 182	16	80.0	434	8	AO359213	AO359213	HS 5029.B
110	16.8	84.0	937	5	EX369467	EX369467	c 183	16	80.0	440	1	AI832063	AI832063	wj9b07.X
111	16.8	84.0	944	7	CF407134	CH3#046.E	c 184	16	80.0	466	2	BF334502	BF334502	QV1-CT036
112	16.8	84.0	946	7	CF407133	CH3#046.E	c 185	16	80.0	468	2	AW294103	AW294103	UI-H-B12
113	16.8	84.0	951	4	BG106993	602291234	c 186	16	80.0	474	1	AI781165	AI781165	EST262044
114	16.8	84.0	953	5	BQ806621	AGENCOURT	c 187	16	80.0	478	1	AI485819	AI485819	EST244140
115	16.8	84.0	956	5	BQ940067	AGENCOURT	c 188	16	80.0	480	1	AI484353	AI484353	EST249001
116	16.8	84.0	957	4	BG107096	602291194	c 189	16	80.0	488	1	AL721570	AL721570	AL721570
117	16.8	84.0	960	4	BG180820	602291258	c 190	16	80.0	489	1	BG960107	BG960107	PM3-CT064
118	16.8	84.0	981	4	BG255231	602369788	c 191	16	80.0	496	1	AA877666	AA877666	rr06B04.S
119	16.8	84.0	1001	4	BQ233792	AGENCOURT	c 192	16	80.0	500	5	CA525088	CA525088	KS2204850
120	16.8	84.0	1053	5	BQ233792	AGENCOURT	c 193	16	80.0	506	2	BQ419590	BQ419590	fa53f103.
121	16.4	82.0	220	8	AZ585577	LM0390A23	c 194	16	80.0	510	2	BE451170	BE451170	EST402058
122	16.4	82.0	359	5	BY082594	BY082594	c 195	16	80.0	510	2	BE344338	BE344338	EST344322
123	16.4	82.0	393	4	BG354109	00616.1ea	c 196	16	80.0	511	1	AI776074	AI776074	EST257270
124	16.4	82.0	412	2	AW450660	UI-M-BH3-	c 197	16	80.0	514	4	CA524361	CA524361	KS12036F0
125	16.4	82.0	431	2	CF914137	030120AEM	c 198	16	80.0	514	4	BI206211	BI206211	EST524251
126	16.4	82.0	439	8	B37080	HS-1042-B1-	c 199	16	80.0	516	2	BE460881	BE460881	EST412300
127	16.4	82.0	449	1	AV635670	AV635670	c 200	16	80.0	518	5	BQ697468	BQ697468	NXPV 056
128	16.4	82.0	468	7	CN9112411	021217ABM	c 201	16	80.0	519	2	BE432539	BE432539	EST299068
129	16.4	82.0	468	7	CN9112440	021217ABM	c 202	16	80.0	523	2	AW096765	AW096765	EST289945
130	16.4	82.0	468	7	CN9112669	030107ABM	c 203	16	80.0	535	5	BM979191	BM979191	UI-CP-DU1
131	16.4	82.0	474	1	AV613781	AV613781	c 204	16	80.0	535	5	BU739679	BU739679	UI-E-EJ0-
132	16.4	82.0	476	1	AV625320	AV625320	c 205	16	80.0	535	6	CS160404	CS160404	K-EST0220
133	16.4	82.0	490	2	BB768373	BB768373	c 206	16	80.0	540	1	AI774552	AI774552	EST255552
134	16.4	82.0	492	7	CN861575	00802AAH	c 207	16	80.0	544	1	AA432108	AA432108	EST255552
135	16.4	82.0	500	6	CD363734	UI-M-GLO-	c 208	16	80.0	544	4	BM065536	BM065536	KS07004F0
136	16.4	82.0	506	5	BQ821725	1030094D1	c 209	16	80.0	558	1	AI782638	AI782638	EST263517
137	16.4	82.0	510	1	AV623759	AV623759	c 210	16	80.0	572	2	BF693663	BF693663	602081846
138	16.4	82.0	520	1	AI119432	ue99b10.Y	c 211	16	80.0	585	7	CR863613	CR863613	34878.1n
139	16.4	82.0	532	2	BE864052	UI-M-BH1-	c 212	16	80.0	586	1	AI484369	AI484369	EST249017
140	16.4	82.0	543	2	BF765273	BF765273	c 213	16	80.0	588	4	BM775102	BM775102	fy50f12.X
141	16.4	82.0	557	2	BQ811599	1030024B0	c 214	16	80.0	596	6	CH112680	CH112680	K-EST0154
142	16.4	82.0	582	8	B2113439	CH230-211	c 215	16	80.0	599	4	BG125352	BG125352	EST470998
143	16.4	82.0	583	9	CR037874	Reverse s	c 216	16	80.0	600	5	BQ047697	BQ047697	EST596815
144	16.4	82.0	604	3	AY068079	Schmidtea	c 217	16	80.0	601	7	BQ113685	BQ113685	EST599261
145	16.4	82.0	611	9	CE027357	tlgr-9ss-	c 218	16	80.0	601	7	CN347172	CN347172	170006001
146	16.4	82.0	613	4	B1528734	1024093A1	c 219	16	80.0	646	5	BQ118982	BQ118982	EST604558
147	16.4	82.0	614	1	AV391699	AV391699	c 220	16	80.0	649	5	BM930870	BM930870	UI-E-EJ0-
148	16.4	82.0	629	5	BM934565	UI-M-BH3-	c 221	16	80.0	650	4	BM713885	BM713885	UI-E-EJ0-
149	16.4	82.0	638	6	CB525294	UI-M-FY0-	c 222	16	80.0	655	1	AI781164	AI781164	EST262043
150	16.4	82.0	645	9	CR167821	Reverse s	c 223	16	80.0	656	3	CR619119	CR619119	full-leng
151	16.4	82.0	652	7	CO427023	UI-M-HW0-	c 224	16	80.0	660	1	AI538755	AI538755	tp56a11.X
152	16.4	82.0	663	5	BQ652958	1112103E0	c 225	16	80.0	660	6	CA449615	CA449615	UI-H-E11-
153	16.4	82.0	668	2	BH425358	BH425358	c 226	16	80.0	666	7	CN215681	CN215681	29504.SUS
154	16.4	82.0	668	4	BG858397	1024057D1	c 227	16	80.0	674	4	BG593197	BG593197	EST491875
155	16.4	82.0	672	6	CB056500	NISC.J117	c 228	16	80.0	675	5	BG623201	BG623201	UI-H-FH1-
156	16.4	82.0	678	4	B1729350	1031104E0	c 229	16	80.0	696	6	CA419823	CA419823	UI-H-FH0-
157	16.4	82.0	702	8	B2005651	oek65b06.	c 230	16	80.0	706	9	CS141473	CS141473	tlgr-gss-
158	16.4	82.0	707	5	BG650865	1112089G0	c 231	16	80.0	719	7	CR862322	CR862322	33476.1n
159	16.4	82.0	721	8	BH954367	oed21h05.	c 232	16	80.0	723	2	AW953712	AW953712	EST365782
160	16.4	82.0	728	1	AI115287	ue95c02.Y	c 233	16	80.0	731	4	BG025435	BG025435	602276323
161	16.4	82.0	732	5	BM947688	UI-M-EG0P	c 234	16	80.0	742	4	BG643439	BG643439	Dario rer
162	16.4	82.0	741	2	BF468250	UI-M-CC0-	c 235	16	80.0	749	9	EX141036	EX141036	BX141036
163	16.4	82.0	760	6	CD352985	UI-M-GLO-	c 236	16	80.0	766	4	BI211049	BI211049	EST536871
164	16.4	82.0	765	9	CL683025	PR10135C	c 237	16	80.0	779	4	BI434110	BI434110	EST536871
165	16.4	82.0	774	2	BF861572	963024E12	c 238	16	80.0	804	5	BU597462	BU597462	AGENCOURT
166	16.4	82.0	790	9	CL653369	PR10133d	c 239	16	80.0	830	8	AO866055	AO866055	nbab0027C
167	16.4	82.0	824	9	EX980104	Reverse s	c 240	16	80.0	831	4	BM684397	BM684397	UI-E-EJ0-
168	16.4	82.0	903	6	CE205165	AGENCOURT	c 241	16	80.0	875	4	BF983818	BF983818	603204643
169	16.4	82.0	933	8	AZ674621	ENTH36TR	c 242	16	80.0	877	2	BE865751	BE865751	601678133
170	16.4	82.0	1016	8	AZ671479	ENTH401TF	c 243	16	80.0	878	4	B1868977	B1868977	603395265

244	16	80.0	901	5	EX327440	EX327440 BX327440	C 317	15.8	79.0	452	6	CA871010	CA871010 K0907B02-
245	16	80.0	929	5	EQ422771	AGENCOURT	C 318	15.8	79.0	453	5	BQ797395	BQ797395 EST 6333
246	16	80.0	1008	5	BX327441	BX327441	C 319	15.8	79.0	456	2	BF110178	BF110178 0n50d08.x
247	16	80.0	1026	4	BM547147	AGENCOURT	C 320	15.8	79.0	457	1	AA985673	AA985673 tr7le05.s
248	16	80.0	1107	7	BU565899	AGENCOURT	C 321	15.8	79.0	461	1	AA681364	AA681364 vr77h05.s
249	15.8	79.0	1146	7	CF729921	UT-M-HEO	C 322	15.8	79.0	465	1	AA675021	AA675021 vm71c05.r
250	15.8	79.0	161	8	AO644267	RPCI93-DP	C 323	15.8	79.0	466	1	AA681416	AA681416 vr4le09.s
251	15.8	79.0	194	8	AZ893720	RPCI-24-1	C 324	15.8	79.0	467	1	AA549196	AA549196 vk85c10.s
252	15.8	79.0	223	8	AZ825455	2M0100112	C 325	15.8	79.0	469	2	BF110186	BF110186 7n50e08.x
253	15.8	79.0	231	5	BQ872945	QGF11B08	C 326	15.8	79.0	473	4	BM237338	BM237338 K0449E05-
254	15.8	79.0	235	5	BQ988883	QGF16C07	C 327	15.8	79.0	476	2	BE334882	BE334882 us90c03.y
255	15.8	79.0	235	5	BQ988883	QGF16C07	C 328	15.8	79.0	478	2	BF653601	BF653601 277479 MA
256	15.8	79.0	235	5	BQ982106	QGE15J02	C 329	15.8	79.0	479	1	AA208869	AA208869 mw75g03.r
257	15.8	79.0	275	5	BQ849023	QGA8M04.y	C 330	15.8	79.0	479	8	BZ855783	BZ855783 CH240.196
258	15.8	79.0	280	5	QX854155	QGB22H22	C 331	15.8	79.0	482	7	CK334756	CK334756 H3105C08-
259	15.8	79.0	282	9	EX893517	ArabiDops	C 332	15.8	79.0	488	1	AA422804	AA422804 vd46d06.s
260	15.8	79.0	283	1	AA647476	vg78a05.s	C 333	15.8	79.0	489	1	AAQ60093	AAQ60093 CIT-HSP-2
261	15.8	79.0	292	1	AA981112	vx57a05.r	C 334	15.8	79.0	491	8	AAQ60135	AAQ60135 CIT-HSP-2
262	15.8	79.0	299	5	BQ981663	QGE14G04	C 335	15.8	79.0	495	1	AA414638	AA414638 vc68d10.s
263	15.8	79.0	300	1	AU114418	AU114418	C 336	15.8	79.0	498	4	BM105605	BM105605 509096 MA
264	15.8	79.0	300	1	AV177530	AV177530	C 337	15.8	79.0	504	1	AA414139	AA414139 vd07h03.s
265	15.8	79.0	300	6	C33281	C33281 Yuji	C 338	15.8	79.0	505	7	CN046340	CN046340 v1_p2.d11
266	15.8	79.0	300	6	C33407	C33407 Yuji	C 339	15.8	79.0	506	1	AA675445	AA675445 vr75a02.s
267	15.8	79.0	300	6	C34433	C34433 Yuji	C 340	15.8	79.0	506	1	AA414609	AA414609 vd09b12.s
268	15.8	79.0	300	6	C35529	C35529 Yuji	C 341	15.8	79.0	506	8	BH766443	BH766443 BMBAC341F
269	15.8	79.0	305	5	BQ847416	BQ847416 QGA2C03.y	C 342	15.8	79.0	507	1	AA684167	AA684167 vm68b02.s
270	15.8	79.0	317	2	BB534994	BB534994	C 343	15.8	79.0	509	1	AA413835	AA413835 vc67d03.s
271	15.8	79.0	323	4	BG790128	BG790128 sse63e07	C 344	15.8	79.0	511	8	AZ353402	AZ353402 LM0092G18
272	15.8	79.0	326	5	EX635762	EX635762	C 345	15.8	79.0	516	5	BQ328332	BQ328332 UI-1-C80-
273	15.8	79.0	329	7	D73357	D73357 CELK117HXR	C 346	15.8	79.0	516	8	AZ606994	AZ606994 LM0429F07
274	15.8	79.0	335	5	BU005141	BU005141 QGG7D22.y	C 347	15.8	79.0	518	5	BH319479	BH319479 603850807
275	15.8	79.0	335	7	D72008	CELK085C7R	C 348	15.8	79.0	522	7	CN668393	CN668393 A0866F02-
276	15.8	79.0	343	1	AA547532	AA547532 vk83c01.s	C 349	15.8	79.0	522	7	BQ595664	BQ595664 E012692-0
277	15.8	79.0	349	1	AA437913	AA437913 vq22b09.s	C 350	15.8	79.0	522	7	CN668393	CN668393 A0866F02-
278	15.8	79.0	360	9	CR032045	CR032045 Reverse s	C 351	15.8	79.0	524	7	CN679489	CN679489 E0125B06-
279	15.8	79.0	370	1	AA107244	AA107244 m158c03.z	C 352	15.8	79.0	524	1	AA647568	AA647568 vq82g03.s
280	15.8	79.0	372	1	AA681645	AA681645 vr43d03.s	C 353	15.8	79.0	526	6	CB478750	CB478750 jns40.p05
281	15.8	79.0	385	4	AA690096	AA690096 vr79b04.s	C 354	15.8	79.0	528	1	AA667022	AA667022 vr86f11.s
282	15.8	79.0	385	4	BI280331	BI280331 UT-R-DEO	C 355	15.8	79.0	528	6	CA895963	CA895963 B0195G03-
283	15.8	79.0	386	1	AA645463	AA645463 vg66g10.s	C 356	15.8	79.0	530	7	CF512166	CF512166 CABud0003-
284	15.8	79.0	387	2	BP455898	BP455898 UT-M-B21	C 357	15.8	79.0	531	2	AW495081	AW495081 UI-M-BH3-
285	15.8	79.0	388	1	AI663763	AI663763 uq47f09.y	C 358	15.8	79.0	533	8	AZ979637	AZ979637 2M0256B21
286	15.8	79.0	390	1	AA647512	AA647512 vq78e04.s	C 359	15.8	79.0	535	5	BQ381970	BQ381970 k48f02.y
287	15.8	79.0	390	5	BQ381831	BQ381831 Kk46g04.y	C 360	15.8	79.0	537	2	B5013903	B5013903 125421 MA
288	15.8	79.0	396	1	AA647743	AA647743 vq79a05.s	C 361	15.8	79.0	538	1	AA726564	AA726564 v441d02.r
289	15.8	79.0	406	6	CB972781	CB972781 CAB30001	C 362	15.8	79.0	542	6	CD550089	CD550089 B0306F11-
290	15.8	79.0	403	9	CR189823	CR189823 Reverse s	C 363	15.8	79.0	543	1	AI791870	AI791870 or7le05.y
291	15.8	79.0	407	1	AA647528	AA647528 vq78f12.s	C 364	15.8	79.0	544	5	BQ381972	BQ381972 k48f05.y
292	15.8	79.0	407	1	AA415456	AA415456 vq99c08.s	C 365	15.8	79.0	549	7	CF512253	CF512253 CABud0003
293	15.8	79.0	409	1	AA681528	AA681528 vr42d10.s	C 366	15.8	79.0	552	1	AA675221	AA675221 vr65c10.s
294	15.8	79.0	411	1	AA413661	AA413661 vc55d07.s	C 367	15.8	79.0	559	6	CA871687	CA871687 K0912D07-
295	15.8	79.0	416	5	BY296265	BY296265 BY296265	C 368	15.8	79.0	559	6	CD539376	CD539376 B0212B10-
296	15.8	79.0	421	1	AA414177	AA414177 vc59e05.s	C 369	15.8	79.0	559	6	CF164401	CF164401 B0742E04-
297	15.8	79.0	422	4	BI783877	BI783877 kh39d12.y	C 370	15.8	79.0	559	6	BQ382240	BQ382240 k443h11.y
298	15.8	79.0	424	1	AA681666	AA681666 vr43f04.s	C 371	15.8	79.0	562	5	BQ382240	BQ382240 k443h11.y
299	15.8	79.0	424	1	AA415342	AA415342 v419b02.s	C 372	15.8	79.0	565	1	AA414261	AA414261 vd08c01.s
300	15.8	79.0	426	6	CB972710	CB972710 CAB30001	C 373	15.8	79.0	565	5	BQ382240	BQ382240 k443h11.y
301	15.8	79.0	428	1	AA422713	AA422713 vq29a04.s	C 374	15.8	79.0	568	5	BQ381742	BQ381742 k443f12.y
302	15.8	79.0	431	2	BF431089	BF431089 7007a08.x	C 375	15.8	79.0	572	8	BH579969	BH579969 BOGLP91TF
303	15.8	79.0	439	6	CA895334	CA895334 B0191D09-	C 376	15.8	79.0	575	7	CK335205	CK335205 H315F11-
304	15.8	79.0	440	5	BY456108	BY456108 BY456108	C 377	15.8	79.0	575	8	CC315602	CC315602 TAM32-2B6
305	15.8	79.0	442	1	AA435257	AA435257 vq49c02.s	C 378	15.8	79.0	576	8	B2160225	B2160225 CH230-484
306	15.8	79.0	443	1	AI476246	AI476246 t172d12.x	C 379	15.8	79.0	577	5	BX113188	BX113188 BX113188
307	15.8	79.0	443	1	AA549304	AA549304 vr75a04.s	C 380	15.8	79.0	590	1	AA895974	AA895974 vx52g08.r
308	15.8	79.0	444	1	AA796270	AA796270 vs98f01.r	C 381	15.8	79.0	592	8	AZ470619	AZ470619 LM0284K14
309	15.8	79.0	444	1	AA435322	AA435322 vq49e10.s	C 382	15.8	79.0	593	8	B2517038	B2517038 BOMQ282TF
310	15.8	79.0	445	1	AA549127	AA549127 vk74d05.s	C 383	15.8	79.0	595	2	AW258283	AW258283 uq32g06.y
311	15.8	79.0	447	1	AA636286	AA636286 vq76c01.s	C 384	15.8	79.0	595	7	CN699225	CN699225 E0418E08-
312	15.8	79.0	447	1	AA623787	AA623787 vq73a11.s	C 385	15.8	79.0	596	7	CF903143	CF903143 A0400H07-
313	15.8	79.0	447	8	AQ406581	AQ406581 HS_5100.A	C 386	15.8	79.0	599	7	CO676063	CO676063 DG42-183f
314	15.8	79.0	449	1	AI733469	AI733469 or7le05.x	C 387	15.8	79.0	606	9	CE031599	CE031599 ti9r-ges-
315	15.8	79.0	450	1	AA415309	AA415309 vc97h01.s	C 388	15.8	79.0	610	9	AQ835260	AQ835260 HS_4811.A
316	15.8	79.0	450	1	AA549298	AA549298 vk85h10.s	C 389	15.8	79.0	614	1	AA536889	AA536889 vJ89d07.r

390	15.8	79.0	618	4	BW711842	UI-E-CL1-	C 463	15.8	79.0	761	4	BI738198	603361625
391	15.8	79.0	619	1	A645446	q66e08.s	C 464	15.8	79.0	763	4	BI731062	603351686
392	15.8	79.0	620	3	A440936	Amigres	C 465	15.8	79.0	764	6	CB571010	AGENCYCOURT
393	15.8	79.0	621	6	CB476080	jsell6.A0	C 466	15.8	79.0	765	4	BI733975	603355504
394	15.8	79.0	622	7	CN537960	UI-M-HSO-	C 467	15.8	79.0	766	4	CF743215	UI-M-GV0-
395	15.8	79.0	623	7	CK350249	hggha22	C 468	15.8	79.0	767	6	CA324538	AGENCYCOURT
396	15.8	79.0	624	7	AK951586	2M0216002	C 469	15.8	79.0	768	5	BU557567	AGENCYCOURT
397	15.8	79.0	625	8	B2523084	BOKEB29TF	C 470	15.8	79.0	769	2	BF608971	MY1 00191
398	15.8	79.0	626	1	AK549665	vk80h11.s	C 471	15.8	79.0	770	2	BN608971	UI-M-HSO-
399	15.8	79.0	627	8	BA363297	CH230-96C	C 472	15.8	79.0	771	7	CN533853	602904863
400	15.8	79.0	628	8	AQ320775	RPC111-92	C 473	15.8	79.0	772	4	BI154682	602904863
401	15.8	79.0	629	8	AQ320775	RPC111-92	C 474	15.8	79.0	773	4	BN048979	v2_p3_r20
402	15.8	79.0	630	8	AQ320775	RPC111-92	C 475	15.8	79.0	774	7	BN702555	BOKEB29TF
403	15.8	79.0	631	8	AQ320775	RPC111-92	C 476	15.8	79.0	775	6	CB319001	AGENCYCOURT
404	15.8	79.0	632	8	AQ320775	RPC111-92	C 477	15.8	79.0	776	8	CR236010	Forward s
405	15.8	79.0	633	8	AQ320775	RPC111-92	C 478	15.8	79.0	777	9	CR236010	Forward s
406	15.8	79.0	634	8	AQ320775	RPC111-92	C 479	15.8	79.0	778	9	CR236010	Forward s
407	15.8	79.0	635	8	AQ320775	RPC111-92	C 480	15.8	79.0	779	9	CR236010	Forward s
408	15.8	79.0	636	8	AQ320775	RPC111-92	C 481	15.8	79.0	780	9	CR236010	Forward s
409	15.8	79.0	637	8	AQ320775	RPC111-92	C 482	15.8	79.0	781	9	CR236010	Forward s
410	15.8	79.0	638	8	AQ320775	RPC111-92	C 483	15.8	79.0	782	9	CR236010	Forward s
411	15.8	79.0	639	8	AQ320775	RPC111-92	C 484	15.8	79.0	783	9	CR236010	Forward s
412	15.8	79.0	640	8	AQ320775	RPC111-92	C 485	15.8	79.0	784	9	CR236010	Forward s
413	15.8	79.0	641	8	AQ320775	RPC111-92	C 486	15.8	79.0	785	9	CR236010	Forward s
414	15.8	79.0	642	8	AQ320775	RPC111-92	C 487	15.8	79.0	786	9	CR236010	Forward s
415	15.8	79.0	643	8	AQ320775	RPC111-92	C 488	15.8	79.0	787	9	CR236010	Forward s
416	15.8	79.0	644	8	AQ320775	RPC111-92	C 489	15.8	79.0	788	9	CR236010	Forward s
417	15.8	79.0	645	8	AQ320775	RPC111-92	C 490	15.8	79.0	789	9	CR236010	Forward s
418	15.8	79.0	646	8	AQ320775	RPC111-92	C 491	15.8	79.0	790	9	CR236010	Forward s
419	15.8	79.0	647	8	AQ320775	RPC111-92	C 492	15.8	79.0	791	9	CR236010	Forward s
420	15.8	79.0	648	8	AQ320775	RPC111-92	C 493	15.8	79.0	792	9	CR236010	Forward s
421	15.8	79.0	649	8	AQ320775	RPC111-92	C 494	15.8	79.0	793	9	CR236010	Forward s
422	15.8	79.0	650	8	AQ320775	RPC111-92	C 495	15.8	79.0	794	9	CR236010	Forward s
423	15.8	79.0	651	8	AQ320775	RPC111-92	C 496	15.8	79.0	795	9	CR236010	Forward s
424	15.8	79.0	652	8	AQ320775	RPC111-92	C 497	15.8	79.0	796	9	CR236010	Forward s
425	15.8	79.0	653	8	AQ320775	RPC111-92	C 498	15.8	79.0	797	9	CR236010	Forward s
426	15.8	79.0	654	8	AQ320775	RPC111-92	C 499	15.8	79.0	798	9	CR236010	Forward s
427	15.8	79.0	655	8	AQ320775	RPC111-92	C 500	15.8	79.0	799	9	CR236010	Forward s
428	15.8	79.0	656	8	AQ320775	RPC111-92	C 501	15.8	79.0	800	9	CR236010	Forward s
429	15.8	79.0	657	8	AQ320775	RPC111-92	C 502	15.8	79.0	801	9	CR236010	Forward s
430	15.8	79.0	658	8	AQ320775	RPC111-92	C 503	15.8	79.0	802	9	CR236010	Forward s
431	15.8	79.0	659	8	AQ320775	RPC111-92	C 504	15.8	79.0	803	9	CR236010	Forward s
432	15.8	79.0	660	8	AQ320775	RPC111-92	C 505	15.8	79.0	804	9	CR236010	Forward s
433	15.8	79.0	661	8	AQ320775	RPC111-92	C 506	15.8	79.0	805	9	CR236010	Forward s
434	15.8	79.0	662	8	AQ320775	RPC111-92	C 507	15.8	79.0	806	9	CR236010	Forward s
435	15.8	79.0	663	8	AQ320775	RPC111-92	C 508	15.8	79.0	807	9	CR236010	Forward s
436	15.8	79.0	664	8	AQ320775	RPC111-92	C 509	15.8	79.0	808	9	CR236010	Forward s
437	15.8	79.0	665	8	AQ320775	RPC111-92	C 510	15.8	79.0	809	9	CR236010	Forward s
438	15.8	79.0	666	8	AQ320775	RPC111-92	C 511	15.8	79.0	810	9	CR236010	Forward s
439	15.8	79.0	667	8	AQ320775	RPC111-92	C 512	15.8	79.0	811	9	CR236010	Forward s
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441	15.8	79.0	669	8	AQ320775	RPC111-92	C 514	15.8	79.0	813	9	CR236010	Forward s
442	15.8	79.0	670	8	AQ320775	RPC111-92	C 515	15.8	79.0	814	9	CR236010	Forward s
443	15.8	79.0	671	8	AQ320775	RPC111-92	C 516	15.8	79.0	815	9	CR236010	Forward s
444	15.8	79.0	672	8	AQ320775	RPC111-92	C 517	15.8	79.0	816	9	CR236010	Forward s
445	15.8	79.0	673	8	AQ320775	RPC111-92	C 518	15.8	79.0	817	9	CR236010	Forward s
446	15.8	79.0	674	8	AQ320775	RPC111-92	C 519	15.8	79.0	818	9	CR236010	Forward s
447	15.8	79.0	675	8	AQ320775	RPC111-92	C 520	15.8	79.0	819	9	CR236010	Forward s
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452	15.8	79.0	680	8	AQ320775	RPC111-92	C 525	15.8	79.0	824	9	CR236010	Forward s
453	15.8	79.0	681	8	AQ320775	RPC111-92	C 526	15.8	79.0	825	9	CR236010	Forward s
454	15.8	79.0	682	8	AQ320775	RPC111-92	C 527	15.8	79.0	826	9	CR236010	Forward s
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459	15.8	79.0	687	8	AQ320775	RPC111-92	C 532	15.8	79.0	831	9	CR236010	Forward s
460	15.8	79.0	688	8	AQ320775	RPC111-92	C 533	15.8	79.0	832	9	CR236010	Forward s
461	15.8	79.0	689	8	AQ320775	RPC111-92	C 534	15.8	79.0	833	9	CR236010	Forward s
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C 682	15.2	76.0	304	7	CK508721	IFND_H08	755	15.2	76.0	426	6	CB329727	3529_1_32
C 683	15.2	76.0	312	8	BH546550	B0CME11TR	C 756	15.2	76.0	428	2	AW237691	xm75910.x
C 684	15.2	76.0	314	2	B8045525	B8045525	757	15.2	76.0	429	6	CB096121	gs09e04.b
C 685	15.2	76.0	317	8	AQ545161	CITBI-EI-	758	15.2	76.0	431	9	C8509645	OS760901
C 686	15.2	76.0	320	7	CR628467	KDFZP4590	759	15.2	76.0	433	9	C8509645	OS760901
C 687	15.2	76.0	321	2	BF552021	UI-R-C2P-	C 760	15.2	76.0	433	2	AW389091	MR2183742
C 688	15.2	76.0	322	4	B8774991	IL2-UM007	761	15.2	76.0	434	2	BE317823	NF059A11L
C 689	15.2	76.0	322	4	B8085736	H3116H05-	C 762	15.2	76.0	434	4	BM316877	fw76b02.y
C 690	15.2	76.0	322	8	BH824805	BACPP21-G	763	15.2	76.0	434	9	CR257611	Reverse.s
C 691	15.2	76.0	324	7	HT1617	YU71H02.r1	764	15.2	76.0	435	4	BI321807	saferse11
C 692	15.2	76.0	329	6	CF041440	QCT66C10.	765	15.2	76.0	436	1	AA578364	nl32C03.s
C 693	15.2	76.0	331	1	A1234760	EST231322	766	15.2	76.0	436	8	AQ033490	HS_-2228.A
C 694	15.2	76.0	335	1	AU284120	AU284120	767	15.2	76.0	436	8	CR262932	Reverse.s
C 695	15.2	76.0	335	9	CG663892	OST450021	C 768	15.2	76.0	437	5	BQ326665	MR2-ST013
C 696	15.2	76.0	339	7	W06537	T2362_MVAT4	769	15.2	76.0	437	8	AZ766231	1M0563P10
C 697	15.2	76.0	343	9	CG493725	OST732165	C 770	15.2	76.0	441	4	BG763423	602735501
C 698	15.2	76.0	344	5	BI190808	BY190808	C 771	15.2	76.0	442	5	BY249936	BY249936
C 699	15.2	76.0	345	6	BY791866	BY791866	C 772	15.2	76.0	443	5	BE947979	UI-M-BH3-
C 700	15.2	76.0	346	5	BQ294139	1991036E0	773	15.2	76.0	444	5	BQ100980	ij2dell.y
C 701	15.2	76.0	350	8	AQ644868	RPCI93-EC	774	15.2	76.0	444	5	BQ101148	ij2dell.y
C 702	15.2	76.0	351	9	CL246650	Q80439-0	C 775	15.2	76.0	445	1	A1154640	ud37a03.r
C 703	15.2	76.0	352	2	BF904082	CM1-MT024	776	15.2	76.0	445	8	CC349842	Q87AE15TV
C 704	15.2	76.0	356	5	BQ148577	NF078D03F	777	15.2	76.0	445	9	CG605166	OST281556
C 705	15.2	76.0	359	8	AZ279488	RPCI-23-1	778	15.2	76.0	445	9	CG660667	OST440759
C 706	15.2	76.0	360	5	BE203119	EST403141	779	15.2	76.0	446	1	AL965278	AL965278
C 707	15.2	76.0	360	5	BY178099	BY178099	C 780	15.2	76.0	446	5	BF873402	BP873402
C 708	15.2	76.0	361	6	CB280834	3529_1_16	C 781	15.2	76.0	446	8	AZ790525	2M0039P01
C 709	15.2	76.0	362	8	AQ099895	HS_3057.A	782	15.2	76.0	449	6	CA872338	K0317A11-
C 710	15.2	76.0	363	8	BZ660497	CH240_269	783	15.2	76.0	449	6	CG596821	OST259493
C 711	15.2	76.0	366	4	BQ070953	H3092E05-	784	15.2	76.0	450	9	BQ101023	ij23a05.y
C 712	15.2	76.0	367	5	BF574357	BF574357	785	15.2	76.0	450	9	CG626947	OST335904
C 713	15.2	76.0	368	7	CK942957	4066692_B	C 786	15.2	76.0	451	1	A2818736	UI-R-10-a
C 714	15.2	76.0	369	4	BQ378112	BQ378112	787	15.2	76.0	451	8	AA162856	mm49d07.r
C 715	15.2	76.0	370	8	AZ244928	RPCI-23-4	788	15.2	76.0	452	1	AA162856	mm49d07.r
C 716	15.2	76.0	371	2	AW743974	ui-26b09.y	789	15.2	76.0	453	9	CG563116	OST186140
C 717	15.2	76.0	371	2	BE987800	UI-M-CG0P	790	15.2	76.0	454	2	BA466317	hx91c08.x
C 718	15.2	76.0	374	4	BQ005951	QV4-GN024	791	15.2	76.0	454	9	CG524314	OST98164
C 719	15.2	76.0	380	8	AZ228832	RPCI-23-9	C 792	15.2	76.0	456	2	BA463146	UI-M-CG0P
C 720	15.2	76.0	382	2	BF640702	NF036E091	793	15.2	76.0	456	2	BA463146	UI-M-CG0P
C 721	15.2	76.0	382	8	AQ558871	HS_2089.B	794	15.2	76.0	457	1	AI536162	mr01f05.y
C 722	15.2	76.0	385	2	BF740590	QV1-HB003	795	15.2	76.0	457	1	AI536162	mr01f05.y
C 723	15.2	76.0	386	8	BH345693	CH230-54B	796	15.2	76.0	458	7	CK615387	LP5m_d16
C 724	15.2	76.0	389	8	B55393	CIT-HSP-386	C 797	15.2	76.0	459	2	AW191694	HIGE05..18
C 725	15.2	76.0	390	6	BY655437	BY655437	798	15.2	76.0	459	6	CB738185	AMGNNUC:N
C 726	15.2	76.0	394	6	CG528149	OST102494	C 799	15.2	76.0	459	6	CSN03PFE	Tetraodon
C 727	15.2	76.0	395	6	CB775968	AMGNNUC:M	C 800	15.2	76.0	462	1	AA464402	ZX77G10.r
C 728	15.2	76.0	395	6	CG511155	OST63304	801	15.2	76.0	462	4	BM162892	EST565415
C 729	15.2	76.0	401	9	CL404395	ZMMBB040	802	15.2	76.0	463	6	BF178970	ma38d04.
C 730	15.2	76.0	402	8	AQ099001	RPCI-23-4	803	15.2	76.0	463	6	CB153037	K-EST0210
C 731	15.2	76.0	402	8	AQ099001	RPCI11-10	804	15.2	76.0	464	1	AV761068	AV761068
C 732	15.2	76.0	404	2	AW494497	UI-M-BH3-	805	15.2	76.0	464	7	CO193170	EC35236.5
C 733	15.2	76.0	404	2	CG553193	OST165429	806	15.2	76.0	465	1	AA137995	mr01f05.y
C 734	15.2	76.0	405	5	BY030272	BY030272	807	15.2	76.0	465	9	CG624360	OST372832
C 735	15.2	76.0	406	7	CK608528	IFNB_N23	808	15.2	76.0	468	7	CK761349	am01-5ms
C 736	15.2	76.0	406	8	BZ782520	A3SP3C72	809	15.2	76.0	468	9	CG567907	OST194513
C 737	15.2	76.0	407	2	AW456243	UI-M-BH3-	810	15.2	76.0	469	2	AW358698	43433_MAR
C 738	15.2	76.0	407	6	CB604971	3529_1_64	811	15.2	76.0	469	9	CG539731	OST131018
C 739	15.2	76.0	409	1	AA231412	ma35G01.r	812	15.2	76.0	471	9	CG596024	OST257183
C 740	15.2	76.0	410	8	BZ313667	hx62a12.g	813	15.2	76.0	472	5	BY244253	BY244253
C 741	15.2	76.0	411	3	GN50A68R	Arabidops	C 814	15.2	76.0	472	8	AQ003947	CIT-HSP-2
C 742	15.2	76.0	411	8	AQ151381	HS_2211.A	815	15.2	76.0	473	2	BF003802	T_brucel
C 743	15.2	76.0	416	6	CB767699	AMGNNUC:N	816	15.2	76.0	473	9	TA31F11Q	AL374038
C 744	15.2	76.0	417	7	CR465897	CR465897	817	15.2	76.0	475	1	AL374038	MBB04C11
C 745	15.2	76.0	419	8	BZ313813	hx64a01.g	818	15.2	76.0	475	5	BX760944	BX760944
C 746	15.2	76.0	420	2	AW388768	MR2-ST013	C 819	15.2	76.0	476	1	AL368782	OSTBA26G03
C 747	15.2	76.0	421	2	BF543699	UI-R-A0-a	820	15.2	76.0	476	9	CG645994	OST391279
C 748	15.2	76.0	421	8	BZ284521	CH230-481	C 821	15.2	76.0	477	5	BY405259	BY405259
C 749	15.2	76.0	422	8	AZ798984	2M0056A12	822	15.2	76.0	478	2	BF644249	NF059C08E
C 750	15.2	76.0	424	5	BQ100702	1J22d11.x	823	15.2	76.0	478	4	BM540150	hb38902.9
C 751	15.2	76.0	424	5	BQ100846	1J24e12.x	824	15.2	76.0	479	5	BY247731	BY247731
C 752	15.2	76.0	426	2	AW389050	MR2-ST013	C 825	15.2	76.0	479	6	CB605150	3529_1_68
C 753	15.2	76.0	426	2	BB728828	BB728828	C 826	15.2	76.0	479	6	CB730968	AMGNNUC:U
C 754	15.2	76.0	426	5	BU080784	sq29C05.	C 827	15.2	76.0	480	1	AA010423	zi09d02.r

C 828	15.2	76.0	481	1	AI127272	AI127272	q870c09.x	901	15.2	76.0	545	7	CR551563	CR551563
829	15.2	76.0	481	9	CG641001	OST374924		902	15.2	76.0	547	5	BU101323	BU101323
830	15.2	76.0	482	4	BM054612	ID53408.Y		903	15.2	76.0	547	6	CB120328	K-EST0167
831	15.2	76.0	483	9	CG635069	OST356837		904	15.2	76.0	547	8	AQ730936	HS-5497_B
832	15.2	76.0	483	9	CG567790	OST194345		905	15.2	76.0	547	9	CE384563	tigr-gss-
833	15.2	76.0	483	9	CG596524	OST258538		906	15.2	76.0	548	8	AQ772067	HS-5475_A
834	15.2	76.0	484	4	EG216934	RG216934		907	15.2	76.0	549	1	AL374039	MtB040C11
835	15.2	76.0	484	9	CG590852	OST244734		908	15.2	76.0	549	8	A2159217	SP-0062_A
836	15.2	76.0	487	1	AJ693337	AJ693337		909	15.2	76.0	550	4	BG019456	del3a05.Y
837	15.2	76.0	487	1	BU045702	PP-Lea002		910	15.2	76.0	550	5	BQ039964	gd29e06.Y
C 838	15.2	76.0	487	5	BU045702	PP-Lea002		911	15.2	76.0	550	5	BQ039964	gd29e06.Y
839	15.2	76.0	487	5	EX483331	DKF2P6860		912	15.2	76.0	551	1	CG577693	OST214158
840	15.2	76.0	488	9	CG600314	OST259621		913	15.2	76.0	551	1	AL779926	AL779926
841	15.2	76.0	488	6	CG575870	OST210069		914	15.2	76.0	551	4	AW141937	EST292052
842	15.2	76.0	489	8	CD527166	CD527166		915	15.2	76.0	551	4	BU196762	BU196762
843	15.2	76.0	489	8	AQ999167	AQ999167		916	15.2	76.0	552	2	AW606685	MRO-HT040
844	15.2	76.0	490	9	CG610032	OST293061		917	15.2	76.0	552	4	BG002758	QV4-GN025
845	15.2	76.0	491	9	CG610072	OST293061		918	15.2	76.0	553	7	CF918516	Eflor458.
846	15.2	76.0	492	9	CG544541	OST141900		919	15.2	76.0	557	8	AZ241318	RPCI-23-8
847	15.2	76.0	493	1	AL603420	DKF2P686G		920	15.2	76.0	558	6	CD178610	MS1-0014P
848	15.2	76.0	493	2	BF093736	BF093736		921	15.2	76.0	558	7	CM107058	EC2CA32CD
849	15.2	76.0	495	8	AQ222344	AQ222344		922	15.2	76.0	559	9	CG585974	OST233914
850	15.2	76.0	500	5	BE431149	SUN011.H1		923	15.2	76.0	561	8	CG569282	OST197217
851	15.2	76.0	500	5	BU209737	603950037		924	15.2	76.0	563	5	BQ40324	gd14c10.Y
852	15.2	76.0	503	4	RG882262	saeg7h12.		925	15.2	76.0	563	6	CF002324	QBH10904.
853	15.2	76.0	504	2	AW078243	fe47a02.Y		926	15.2	76.0	564	1	AI137350	UI-R-C2p-
854	15.2	76.0	505	7	CF897127	CF897127		927	15.2	76.0	564	4	BM743787	K-EST0017
855	15.2	76.0	506	5	BN960437	BN960437		928	15.2	76.0	564	6	CB086913	h192d11.g
856	15.2	76.0	507	8	AQ992827	RPCI-23-3		929	15.2	76.0	565	8	AQ292547	RPCI-23-2
857	15.2	76.0	508	2	BE198095	u979d04.x		930	15.2	76.0	566	6	CB834061	3529-1.87
858	15.2	76.0	509	6	CB275574	pk99h04.Y		931	15.2	76.0	566	6	CD484684	3529-1.11
859	15.2	76.0	510	1	AI138641	ml10e11.Y		932	15.2	76.0	567	7	CR823046	1j23d11.x
860	15.2	76.0	511	4	BJ161260	BJ161260		933	15.2	76.0	567	6	CB885715	3529-1.89
861	15.2	76.0	512	9	CG607331	CG607331		934	15.2	76.0	568	2	BF636842	NF047C06L
862	15.2	76.0	513	9	BU161051	BU161051		935	15.2	76.0	568	4	BJ627230	BJ627230
863	15.2	76.0	514	9	CG536140	OST123769		936	15.2	76.0	569	4	BG763646	602735864
864	15.2	76.0	515	7	CM281917	170004241		937	15.2	76.0	569	9	CR823047	1j23d11.Y
865	15.2	76.0	515	9	CG620520	OST17751		938	15.2	76.0	569	9	CA991431	Reverse.s
866	15.2	76.0	516	9	CG539875	CG539875		939	15.2	76.0	571	6	CA991431	EST644939
867	15.2	76.0	517	8	AQ978737	RPCI-23-3		940	15.2	76.0	572	2	BF003572	EST432070
868	15.2	76.0	517	7	CM282323	CM282323		941	15.2	76.0	572	7	U44984	U44984
869	15.2	76.0	519	9	CG587888	CG587888		942	15.2	76.0	573	1	AI138911	mr10e11.r
870	15.2	76.0	520	4	BG364870	dg92f05.Y		943	15.2	76.0	574	6	CB274360	mai90g11.
871	15.2	76.0	521	1	AA600000	ag29g09.s		944	15.2	76.0	575	8	BS466639	BS466639
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873	15.2	76.0	521	5	AX219758	EST302240		946	15.2	76.0	578	8	AQ285526	RPCI-23-2
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877	15.2	76.0	523	9	CG582325	CG582325		950	15.2	76.0	582	5	BA265312	BA265312
878	15.2	76.0	524	6	CF023138	CF023138		951	15.2	76.0	582	8	AZ098559	RPCI-23-4
879	15.2	76.0	524	9	CG664086	CG664086		952	15.2	76.0	583	4	BM731409	BM731409
880	15.2	76.0	525	7	CM624060	CM624060		953	15.2	76.0	583	6	CB281937	CB281937
881	15.2	76.0	527	1	AV994061	AV994061		954	15.2	76.0	584	3	CB586503	CB586503
882	15.2	76.0	527	4	BS358909	BS358909		955	15.2	76.0	584	7	BI270351	BI270351
883	15.2	76.0	527	9	CL195807	CL195807		956	15.2	76.0	585	4	BM765996	BM765996
884	15.2	76.0	530	1	AJ695907	AJ695907		957	15.2	76.0	586	4	BM765996	K-EST0047
885	15.2	76.0	530	8	AQ187859	AQ187859		958	15.2	76.0	586	8	AZ646583	AZ646583
886	15.2	76.0	531	7	CM679982	CM679982		959	15.2	76.0	587	6	CD670214	CD670214
887	15.2	76.0	531	9	CG566371	OST195337		960	15.2	76.0	588	3	AY104692	AY104692
888	15.2	76.0	532	9	CG670125	CG670125		961	15.2	76.0	588	9	CE281206	CE281206
889	15.2	76.0	533	8	AQ2070719	RPCI-23-4		962	15.2	76.0	591	2	BF719273	mab38d04.
890	15.2	76.0	533	9	CG524646	CG524646		963	15.2	76.0	592	5	BQ520998	BQ520998
891	15.2	76.0	534	4	BM567758	BM567758		964	15.2	76.0	593	8	BZ195974	BZ195974
892	15.2	76.0	534	6	CB718348	CB718348		965	15.2	76.0	594	2	AK373052	AK373052
893	15.2	76.0	535	1	AU180719	AU180719		966	15.2	76.0	595	2	AW898996	AW898996
894	15.2	76.0	535	7	CK234959	CK234959		967	15.2	76.0	595	2	AW898072	RC3-NN006
895	15.2	76.0	536	6	CD058739	CD058739		968	15.2	76.0	595	2	BE614704	BE614704
896	15.2	76.0	538	5	BF122604	BF122604		969	15.2	76.0	595	7	CL210785	CL210785
897	15.2	76.0	542	4	BS894448	BS894448		970	15.2	76.0	596	9	CD537895	CD537895
898	15.2	76.0	542	7	CM623766	CM623766		971	15.2	76.0	596	6	CD058969	CD058969
899	15.2	76.0	543	6	CD548003	CD548003		972	15.2	76.0	598	7	CK310625	CK310625
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974 15.2 76.0 599 5 BWO29954 BWO29954
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981 15.2 76.0 604 2 BF754317 BF754317
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985 15.2 76.0 605 7 BF718964 BF718964
986 15.2 76.0 607 6 BY724318 BY724318
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989 15.2 76.0 609 7 CN716357 CN716357
990 15.2 76.0 610 7 CF894640 CF894640
991 15.2 76.0 610 7 CK764477 CK764477
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993 15.2 76.0 611 7 CK768062 CK768062
994 15.2 76.0 612 2 BF020008 BF020008
995 15.2 76.0 613 8 AZ363972 AZ363972
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997 15.2 76.0 615 9 CC479959 CC479959
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ALIGNMENTS

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RESULT 1
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LOCUS taf55b05.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3'
DEFINITION similar to TR:Q9VAK0 Q9VAK0 CG7568 PROTEIN.; mRNA sequence.
ACCESSION CN633741
VERSION CN633741.1 GI:47144818
KEYWORDS EST.
SOURCE Hydra magnipapillata
ORGANISM Hydra magnipapillata
Eukaryota; Metazoa;
Hydridae; Hydra.

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REFERENCE 1 (bases 1 to 187)
Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
WashU Hydra EST Project
Unpublished (2002)
Contact: Hans Bode

```

```

WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hnbode@uci.edu)
Trace considered overall poor quality
Seq primer: degenerate primer
High quality sequence stop: 1.
Location/Qualifiers
1. 187
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"

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FEATURES

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source
1. 187
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"

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/lab_host="TransformMax EC100 (Epicentre), T1 Phage
resistant electrocompetent cells"
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Site_2: EcoRI"

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ORIGIN

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Query Match 87.0%; Score 17.4; DB 7; Length 187;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 CAGTTAATGGAGAGTGGCT 20
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Db 123 CAGTTAATGGAGAGTGGCT 105
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RESULT 2

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CN771770/c

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LOCUS CN771770 338 bp mRNA linear EST 20-MAY-2004
DEFINITION tad94d07.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3'
similar to TR:Q9VAK0 Q9VAK0 CG7568 PROTEIN.; mRNA sequence.
ACCESSION CN771770
VERSION CN771770.1 GI:47542404
KEYWORDS EST.
SOURCE Hydra magnipapillata
ORGANISM Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.

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REFERENCE 1 (bases 1 to 338)

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Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
WashU Hydra EST Project
Unpublished (2002)
Contact: Hans Bode

```

```

WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hnbode@uci.edu)
Putative full length read
vector to vector length is
Seq primer: degenerate primer.
Location/Qualifiers
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resistant electrocompetent cells"
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/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"

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TITLE

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JOURNAL
COMMENT

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FEATURES

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source

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FEATURES

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source

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Query Match 87.0%; Score 17.4; DB 7; Length 338;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 CAGTTAATGGAGAGTGGCT 20
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Db 249 CAGTTAATGGAGAGTGGCT 231
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RESULT 3
CN772025
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

357 bp mRNA linear EST 20-MAY-2004
tad94d07.y1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 5'
similar to TR:Q9VAK0 Q9VAK0 CG7568 PROTEIN. ; mRNA sequence.

1 GI:47542659
EST.
Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 357)
Bode H., Blumberg B., Steele R., Wigge P., Gee L., Nguyen Q.,
Martinez D., Kibler D., Hampson S., Clifton S., Pape D., Marra M.,
Hillier L., Martin J., Wylie T., Dante M., Theising B., Bowers Y.,
Gibbons M., Ritter E., Bennett J., Ronko I., Tsagareishvili R.,
Maguire L., Kennedy S., Waterston R. and Wilson R.
WashU Hydra EST Project
Unpublished (2002)
Other ESTs: tad94d07.x1
Contact: Hans Bode
WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
Please contact: Hans Bode (hrbode@uci.edu)
Putative full length read
vector to vector length is
Seq primer: -40UP
High quality sequence stop: 357.

1.357
Location/Qualifiers
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"
/lab_host="TransformMax EC100 (Epicentre), T1 Phage
resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"

Query Match 87.0%; Score 17.4; DB 7; Length 357;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAGTTAATGGAGAGTGGCT 20
|||||
Db 88 CAGTTAATGGAGAGTGGCT 106

RESULT 4
CN634000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

381 bp mRNA linear EST 12-MAY-2004
tad55b05.y1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 5'
similar to TR:Q9VAK0 Q9VAK0 CG7568 PROTEIN. ; mRNA sequence.

1 GI:47145077
EST.
Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 381)
Bode H., Blumberg B., Steele R., Wigge P., Gee L., Nguyen Q.,

Query Match 87.0%; Score 17.4; DB 7; Length 357;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAGTTAATGGAGAGTGGCT 20
|||||
Db 88 CAGTTAATGGAGAGTGGCT 106

RESULT 5
BE102024
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

427 bp mRNA linear EST 13-JUN-2000
UI-R-B01-age-d-07-0-UI-s1 UI-R-B01 Rattus norvegicus cDNA clone
UI-R-B01-age-d-07-0-UI 3', mRNA sequence.

BE102024 GI:8494122
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
1 (bases 1 to 427)
Bonaldo M.F., Lennon G. and Soares M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aqe-d-07-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library (UI-R-B01) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_TISSUE=corpus-striatum
TAG_LIB=UI-R-B01
TAG_SEQ=CTAGG"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 427;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CAGTTAATGGAGAGTGGCT 20
||||| ||||||| |||||
DB 370 CAGTTACTGGAGAGTGGCT 388

RESULT 6

LOCUS CN772716 435 bp mRNA linear EST 20-MAY-2004
DEFINITION tae06d02.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3', similar to TR:Q9VAKO Q9VAKO CG7568 PROTEIN. /, mRNA sequence.
ACCESSION CN772716
VERSION CN772716.1 GI:47543350
KEYWORDS EST.
SOURCE Hydra magnipapillata
ORGANISM Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
REFERENCE 1 (bases 1 to 435)
AUTHORS Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q., Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wyllie,F., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Konko,I., Tsagaris,I., R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
TITLE WashU Hydra EST Project
JOURNAL Unpublished (2002)
COMMENT Other ESTs: tae06d02.y1
Contact: Hans Bode
WashU Hydra EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell

Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrobode@uci.edu)
Seq primer: degenerate primer
High quality sequence stop: 407.
Location/Qualifiers
1..435
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre)", T1 Phage resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site 1: NotI; Site 2: EcoRI"

FEATURES

source
1..435
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre)", T1 Phage resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site 1: NotI; Site 2: EcoRI"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 435;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CAGTTAATGGAGAGTGGCT 20
||||| ||||||| |||||
DB 230 CAGTTAATGGAGAGTGGCT 212

RESULT 7

LOCUS A1178866 436 bp mRNA linear EST 20-JAN-1999
DEFINITION EST222548 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone RSPBQ40 3' end, mRNA sequence.
ACCESSION A1178866
VERSION A1178866.1 GI:3729504
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 436)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat Gene Index

JOURNAL

Unpublished (1998)
COMMENT The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlsec@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..436
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2034859"
/db_xref="taxon:10118"
/clone="RSPBQ40"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI"

FEATURES

source
1..436
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2034859"
/db_xref="taxon:10118"
/clone="RSPBQ40"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI"

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 436;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CAGTTAATGGAGAGTGGCT 20
||||| ||||||| |||||
DB 282 CAGTTACTGGAGAGTGGCT 300

Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer
High quality sequence stop: 515.
Location/Qualifiers
1. .517
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"
/la5_host="transformMax EC100 (Epicentre), T1 Phase
resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"
2 2 CAGTTAATGGAGAGTGGCT 20
|||||||
36 CAGTTAATGGAGAGTGGCT 238
|||||||
Ch 87.0%; Score 17.4; DB 7; Length 517;
Similarity 94.7%; Pred. No. 5.6e+02;
18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CN777963 540 bp mRNA linear EST 20-MAY-2004
taf71a06.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3'
similar to TR:Q9VAKO Q9VAKO CG7568 PROTEIN. ;, mRNA sequence.
CN777963
CN777963.1 GI:47548597
EST.
Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 540)
Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Teagareishvili,R.,
Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
WashU Hydra EST Project
Unpublished (2002)
Other_ESTs: taf71a06.y1
Contact: Hans Bode
WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer
High quality sequence stop: 534.
Location/Qualifiers
1. .540
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
/db_xref="taxon:6085"
/la5_host="transformMax EC100 (Epicentre), T1 Phase
resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"

FEATURES	source
ORIGIN	
Query Match	
Best Local	
Matches	
Qy	
Db	2
RESULT 10	
CN777963/c	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	source

linear EST 11-APR-2003
774) Rattus norvegicus
e.

tebrata; Euteleostomi;
; Muridae; Murinae;

01320-1799, USA

Length 462;
Indels 0; Gaps 0;

" I; Site_2: NotI; rat

linear EST 03-MAY-2004
gnipapillata cDNA 3'
...; mRNA sequence.

droida; Anthomedusae;

Gee L., Nguyen,Q.,
n.S., Page,D., Marra,M.,
Theising,B., Bowers,Y.,
., Tsagarisvlii,R.,
llison,R.

uis, MO 63109, USA

GATC Konstanz, Germany
ein / Molecular Cell

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 540;
Best Local Similarity 94.7%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGCT 20
|||||
Db 248 CAGTTAATGGAGAGTGCT 230

RESULT 11

AW526046 550 bp mRNA linear EST 06-MAR-2000
LOCUS
DEFINITION UI-R-B01-aiy-f-05-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone
ACCESSION UI-R-B01-aiy-f-05-0-UI 3', mRNA sequence.
VERSION
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)

EST.
AW526046.1 GI:7168431

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 550)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery

MEDLINE Genome Res. 6 (9), 791-806 (1996)

PUBMED 97044477

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized medulla library cDNA library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

Location/Qualifiers
1..550
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-B01-aiy-f-05-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: p77TD-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
rategst.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG TISSUE=medulla
TAG_LIB=UI-R-B01
TAG_SEQ=GAACCG"

Query Match 87.0%; Score 17.4; DB 2; Length 550;
Best Local Similarity 94.7%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGCT 20
|||||
Db 370 CAGTTAATGGAGAGTGCT 388

RESULT 12

CB613159 557 bp mRNA linear EST 07-APR-2003
LOCUS
DEFINITION AMGNNUC.NRHY7-00021-C9-A nrhy7 (10850) Rattus norvegicus cDNA clone
ACCESSION nrhy7-00021-99 5', mRNA sequence.
VERSION
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)

EST.
CB613159.1 GI:29573047

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 557)

AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00021 row: 9 column: 9.

FEATURES

source

Location/Qualifiers
1..557
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy7-00021-99"
/clone_lib="nrhy7 (10850)"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
hypothalamus adult female WiStar rat avg. Insert size 2.3
kb fraction 6 and 7"

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 557;
Best Local Similarity 94.7%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGCT 20
|||||
Db 527 CAGTTAATGGAGAGTGCT 545

RESULT 13

BF563085 593 bp mRNA linear EST 12-DEC-2000
LOCUS
DEFINITION UI-R-B01-aiy-f-05-0-UI.r1 UI-R-B01 Rattus norvegicus cDNA clone
ACCESSION UI-R-B01-aiy-f-05-0-UI 5', mRNA sequence.
VERSION
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)

EST.
BF563085.1 GI:11672815

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 593)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery

MEDLINE Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1797847
Seq primer: M13 Forward.
Location/Qualifiers
1. .593
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-f-05-0-UI"
/dev_stage="adult"
/lab_host="DHI10B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B01) is a substracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratseq.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 593;
Best Local Similarity 94.7%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
512 CAGTTACTGGAGAGTGGCT 494

Db

RESULT 14
BJ578386/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ578386 673 bp mRNA linear EST 18-DEC-2002
BJ578386 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm38c04 3', mRNA sequence.

BJ578386
BJ578386.1 GI:27260214
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 673)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTs of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .673
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="jm35807"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

FEATURES
source

Query Match 87.0%; Score 17.4; DB 2; Length 705;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
443 CAGTTAATGGAGAGTGGCT 461

Db

RESULT 16
BJ572384/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ572384 740 bp mRNA linear EST 18-DEC-2002
BJ572384 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm20117 3', mRNA sequence.

BJ572384
BJ572384.1 GI:27254212
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1797847
Seq primer: M13 Forward.
Location/Qualifiers
1. .593
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-f-05-0-UI"
/dev_stage="adult"
/lab_host="DHI10B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B01) is a substracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratseq.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 593;
Best Local Similarity 94.7%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
512 CAGTTACTGGAGAGTGGCT 494

Db

RESULT 14
BJ578386/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ578386 673 bp mRNA linear EST 18-DEC-2002
BJ578386 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm38c04 3', mRNA sequence.

BJ578386
BJ578386.1 GI:27260214
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 673)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTs of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .673
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="jm35807"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

FEATURES
source

Query Match 87.0%; Score 17.4; DB 4; Length 705;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
443 CAGTTAATGGAGAGTGGCT 461

Db

RESULT 16
BJ572384/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ572384 740 bp mRNA linear EST 18-DEC-2002
BJ572384 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm20117 3', mRNA sequence.

BJ572384
BJ572384.1 GI:27254212
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1797847
Seq primer: M13 Forward.
Location/Qualifiers
1. .593
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-f-05-0-UI"
/dev_stage="adult"
/lab_host="DHI10B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B01) is a substracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratseq.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 87.0%; Score 17.4; DB 4; Length 705;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
443 CAGTTAATGGAGAGTGGCT 461

Db

RESULT 16
BJ572384/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ572384 740 bp mRNA linear EST 18-DEC-2002
BJ572384 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm20117 3', mRNA sequence.

BJ572384
BJ572384.1 GI:27254212
EST.
Ipomoea nil (Japanese morning glory)
Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;<


```

Db      371 CAGTTACTGGAGAGTGCGC 389
||||| ||||| ||||| ||||| |||||
RESULT 19
CF283555
LOCUS   CF283555
DEFINITION AGENCOURT_15207692 NICHD_XGC_Sp1 Xenopus laevis cDNA clone
IMAGS:5506637 5', mRNA sequence.
ACCESSION CF283555
VERSION   CF283555.1 GI:33643334
KEYWORDS EST.
SOURCE   Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 754)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapps-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12151 row: i column: 06
High quality sequence stop: 679.
Location/Qualifiers
1..754
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5506637"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Sp1"
/notes="Organ: Spleen; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.4 kb. Constructed by Life
Technologies."
ORIGIN
Query Match 87.0%; Score 17.4; DB 6; Length 754;
Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCAGTTAATGGAGAGTGCGC 19
||||| ||||| ||||| ||||| |||||
Db      717 GAAGTTAATGGAGAGTGCGC 735
||||| ||||| ||||| ||||| |||||
RESULT 20
BJ570457/c
LOCUS   BJ570457/c
DEFINITION BJ570457 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm8j16 3', mRNA sequence.
ACCESSION BJ570457
VERSION   BJ570457.1 GI:27252285
KEYWORDS EST.
SOURCE   Ipomoea nil (Japanese morning glory)
ORGANISM Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 757)

AUTHORS Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTs of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..775
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35983"
/clone="jm8j16"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

ORIGIN
Query Match 87.0%; Score 17.4; DB 4; Length 775;
Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCAGTTAATGGAGAGTGCGC 19
||||| ||||| ||||| ||||| |||||

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AUTHORS Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTs of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..775
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35983"
/clone="jm8j16"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

ORIGIN
Query Match 87.0%; Score 17.4; DB 4; Length 757;
Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCAGTTAATGGAGAGTGCGC 19
||||| ||||| ||||| ||||| |||||
Db      290 GCAGTTGATGGAGAGTGCGC 272
||||| ||||| ||||| ||||| |||||
RESULT 21
BJ570485/c
LOCUS   BJ570485/c
DEFINITION BJ570485 Ipomoea nil mixture of flower and flower bud Ipomoea nil
cDNA clone jm8k23 3', mRNA sequence.
ACCESSION BJ570485
VERSION   BJ570485.1 GI:27252313
KEYWORDS EST.
SOURCE   Ipomoea nil (Japanese morning glory)
ORGANISM Ipomoea nil
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
1 (bases 1 to 775)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T.,
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTs of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..775
/organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35983"
/clone="jm8k23"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"

ORIGIN
Query Match 87.0%; Score 17.4; DB 4; Length 775;
Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GCAGTTAATGGAGAGTGCGC 19
||||| ||||| ||||| ||||| |||||

```

285 GCAGTTGATGGAGAGTGGC 267

Db

RESULT 22
CK163790/c

LOCUS
DEFINITION
CK163790
VERSION
CK163790.1 GI:38994382
KEYWORDS
SOURCE
ORGANISM

CK163790
FGAS016424 Triticum aestivum FGAS: Library 4 Gate 8 Triticum
aestivum cDNA, mRNA sequence.

CK163790
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 1091)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, S7 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.estscs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [37,799].
Plate: LAB009 row: D column: 07.

FEATURES
source
location/Qualifiers
1..1091
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
/notes="Organ: Crown and leaf; Vector: pCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% ProMix) in a
growth chamber for 7 days under an irradiance of 200 mmol
m-2 sec-1. The temperature was maintained at 20 degrees C
with a 15-hr photoperiod under a relative humidity of 70%.
After this period watering of plants was stopped. Four
time points were sampled during a two week period; the
first after wilting was observed and the last, two weeks
later, consisted of live crown and leaf tissue (leaf
tissue that was yellow was not included in sampled
material). First strand synthesis in this library was done
in the presence of methylated dCTP thereby protecting from
internal cleavage with NotI."

ORIGIN
Query Match 87.0%; Score 17.4; DB 7; Length 1091;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGC 19
|||||
Db 64 CCAGGTAATGGAGAGTGGC 46
|||||

RESULT 23
AG612934/c

LOCUS
DEFINITION
AG612934
VERSION
AG612934.1 GI:48373764
KEYWORDS
SOURCE
ORGANISM

AG612934
AG612934.1 GI:48373764
GSS.
Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMG01
Unpublished
2 (bases 1 to 1462)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMG01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
location/Qualifiers
1..1462
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMG01-548K03.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

ORIGIN
Query Match 87.0%; Score 17.4; DB 9; Length 1462;
Best Local Similarity 94.7%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGC 19
|||||
Db 1385 GCATTTAATGGAGAGTGGC 1367
|||||

RESULT 24
AY325247/c

LOCUS
DEFINITION
AY325247
VERSION
AY325247.1 GI:33086671
KEYWORDS
SOURCE
ORGANISM

AY325247
Rattus norvegicus Cc2-27 mRNA, complete cds.
AY325247
HNC.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 3276)
Xu, C.S., Li, W.Q., Li, Y.C., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,
Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J.,
Yan, H.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Liver regeneration after PH
Unpublished
REFERENCE
2 (bases 1 to 3276)
Xu, C.S., Li, W.Q., Li, Y.C., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,

Wang,S.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J.,
Yan,H.M., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Direct Submission
Submitted (17-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China

FEATURES source

Location/Qualifiers
1. .3276
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"

CDS

1. .3270
/notes="liver regeneration-related protein LRRG170"
/codon_start=1
/product="Cc2-27"
/protein_id="AAP92648.1"
/db_xref="GI:33086672"
/translations="MDQKTPANSRASSPQCEFEQFIPTVETPYLARAGNEFLNL
VPDIEVRAGSVSKGYLHFKPLSSNWKAFVVRPVFYNSDKDPVGRGIINL
STAQVEYSEDQAMLKTPNTFAVTKHGVLLQALNDKMDWLYAFNLLAGTIRAD
IALGLAVMGONLILNMNDHGFVVCANRTVSKVDDFLAKEAGTKVIGAKSLKMVS
KLKPRVILVRAGQAVDDFIEKLPLDGTBIIIDGNSEYRDTTRCQDLKAKGI
LFVSGSVGSEEGARYGSLMPGCKNEAMPHIKTIFQIAAKVGTGEPCCDWASSGLP
IDCAYHLMKDVLGWRHEEMAQAFEDWNKTELDSELTETANILKFQDTDKELLKIR
DSAGOKTGWTAISALEYGMPTVLGEAVFARCLSLKEERVOAERKLKPKMVKLE
GSKQAFLEDRKALYASAKIISVAGFMLLRQAATERFQWTLNYYGIALMRGCIIRSV
FLGKIDAFENFELQNLDDFFKSAVDQDSWRVISTGVQACIPNCPITLSP
YDGYRHELPANLIIQARDYFGAHTYELLISKPGFTHNTWTHGGRGGRKEEKEE
EEEEEEEEEEEEEEEEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
VEAEQQQYHQRKIAAHHVYVGCQVELDKQVHLGSKQTAAISVETFLAGTENFA
KDLMPARHAKRTITTDVKLLRSLNSLCTVDSVGTEDSVSDSVTSDSVGTEDSV
VGTEDSVTSDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSV
VGTEDSVTSDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSV
SVTSDSVTSDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSVGTEDSV
GDRSLPPPPGRRHRRPQCELSSVRLAVVSDMSWCSKKAERVSLRLAVRVVITLC
F"

ORIGIN

Query Match 87.0%; Score 17.4; DB 3; Length 3276;
Best Local Similarity 94.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CAGTAAATGAGAGTGGCT 20

||||| |||||||
Db 218 CAGTTACTGAGAGTGGCT 200

RESULT 25

BZ224094

LOCUS

DEFINITION BZ224094 645 bp DNA linear GSS 11-OCT-2002
CH230-313K4.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone

REFERENCE BZ224094 1 GI:23882452

ACCESSION

BZ224094

VERSION

BZ224094.1

KEYWORDS

GSS.

SOURCE

Rattus norvegicus

(Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 645)

REFERENCE

Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,

Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,

Riggs,F., de Jong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 MboI segment

Unpublished (1999)

Other_GSSs: CH230-313K4.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end

plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 313 row: K column: 4

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .645
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-313K4"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN

Query Match 85.0%; Score 17; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTAATGAGAGTGGCT 20

||||| |||||||
Db 3 GTTAATGAGAGTGGCT 19

RESULT 26

AG169335/c

LOCUS

DEFINITION

Pan troglodytes DNA, clone: RP43-037P16.T7, genomic survey

sequence.

AG169335

VERSION

AG169335.1

GI:16699013

KEYWORDS

GSS.

SOURCE

Pan troglodytes

(chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of Library RPCI-43

Unpublished

2 (bases 1 to 654)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. .654

/organism="Pan troglodytes"

```

/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-037P16.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

Db
||||| 606 GTTAATGGAGAGTGGCT 622

RESULT 28
BX169283/c
LOCUS
DEFINITION
BX169283
ACCESSION
BX169283.1 GI:28000988
VERSION
GSS:
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 729)
Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 155N24. 155N24
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source
location/Qualifiers
1..729
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="DKEY-155N24"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"
ORIGIN
Query Match 85.0%; Score 17; DB 9; Length 729;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
|||||
Db 235 CAGTTAATGGAGAGTGG 219

RESULT 29
BX169508/c
LOCUS
DEFINITION
BX169508
ACCESSION
BX169508.1 GI:28001213
VERSION
GSS:
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 808)
Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 172C16. 172C16
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source
location/Qualifiers
1..808
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="DKEY-172C16"
QY

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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-037P16.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

Db
||||| 518 GTTAATGGAGAGTGGCT 502

RESULT 27
BZ164877
LOCUS
DEFINITION
CH230-246A22.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-246A22, genomic survey sequence.
ACCESSION
BZ164877
VERSION
BZ164877.1 GI:23805905
KEYWORDS
GSS:
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 683)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-246A22.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.html). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
Plate: 246 row: A column: 22
Seq primer: T7
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..683
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-246A22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
Pieter de Jong"
ORIGIN
Query Match 85.0%; Score 17; DB 8; Length 683;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAATGGAGAGTGGCT 20

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/tissue_type="Testis"
/note="vector pindigoBAC-536"

ORIGIN
Query Match      85.0%; Score 17; DB 9; Length 808;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
|||||
Db 247 CAGTTAATGGAGAGTGG 231

RESULT 30
CB684683
LOCUS OSJNEf14H05.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEf14H05 5', mRNA sequence.
ACCESSION CB684683
VERSION CB684683.1 GI:29688408
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 812)
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,B.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: H column: 05
Seq primer: gta aaa cga cgg cca gtg.
FEATURES
source
location/Qualifiers
1..812
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="OSJNEf14H05"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN
Query Match      85.0%; Score 17; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
|||||
Db 593 CAGTTAATGGAGAGTGG 609

RESULT 31
AW080408/c
LOCUS AW080408
DEFINITION xes3a08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2611574 3',

/tissue_type="Testis"
/note="vector pindigoBAC-536"

ORIGIN
Query Match      85.0%; Score 17; DB 9; Length 808;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
|||||
Db 247 CAGTTAATGGAGAGTGG 231

RESULT 30
CB684683
LOCUS OSJNEf14H05.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEf14H05 5', mRNA sequence.
ACCESSION CB684683
VERSION CB684683.1 GI:29688408
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 812)
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,B.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: H column: 05
Seq primer: gta aaa cga cgg cca gtg.
FEATURES
source
location/Qualifiers
1..812
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="OSJNEf14H05"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN
Query Match      85.0%; Score 17; DB 6; Length 812;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
|||||
Db 593 CAGTTAATGGAGAGTGG 609

RESULT 31
AW080408/c
LOCUS AW080408
DEFINITION xes3a08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2611574 3',

/mRNA sequence.
AW080408
VERSION AW080408.1 GI:6035560
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 200.
location/Qualifiers
1..248
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2611574"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 248;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20
|||||
Db 176 GCTGTTAATGGAGAGTGCT 157

RESULT 32
CN210935/c
LOCUS CN210935
DEFINITION Rt_fcd_00G02_M13-F Cadmium exposed rainbow trout subtractive
Oncorhynchus mykiss cDNA clone Rt_fcd_00G02 5', mRNA sequence.
ACCESSION CN210935
VERSION CN210935.1 GI:46264785
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 249)
AUTHORS Hurley,A.L., Sweeney,G.E. and Kille,P.
TITLE Molecular Genetic Effects of Cadmium Toxicity on Rainbow Trout
Development
JOURNAL Unpublished (2004)
COMMENT Contact: Anna Hurley
Dr Pete Kille
Cardiff University
Museum Ave, BIOSI 2
Tel: +44 02920876703
```

Email: HurlerA@cf.ac.uk

PCR Primers

FORWARD: M13

BACKWARD: M13

Plate: 00 row: G column: 02

Seq primer: M13-F

High quality sequence start: 16

High quality sequence stop: 237.

Location/Qualifiers

FEATURES

source

1..249

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/strain="Upwey Seven-Spring"

/db_xref="taxon:8022"

/clone="Rt fcd 00G02"

/sex="Female"

/clone_lib="Cadmium exposed rainbow trout subtractive"

/note="A subtractive cDNA library was produced to identify

genes that appear up-regulated in response to cadmium

toxicity. Technique was performed using the Clontech PCR

Select cDNA Subtraction Kit, using mRNA from control

(unpolluted) and cadmium exposed (65.7ug/L) 54-day old

rainbow trout."

/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CN0-bml-a-02-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CN0"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CN0
library is a normalized library constructed from the
following tissues: brown adipose, penis, salivary glands,
bladder, fundus, cervix, seminal vesicles. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratesat.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG TISSUE=bladder
TAG LIB=UI-R-CN0
TAG_SEQ=AGC"

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 333;
Best Local Similarity 90.0%; Pred. No. 1.le+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20

||||| ||||| ||||| ||||| |||||

Db 248 GCAGTAGATGGAGAGTGGCT 229

RESULT 34

BE841809

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BE841809 339 bp mRNA linear EST 22-SEP-2000
MR1-SN0065-220500-006-d05 SN0065 Homo sapiens cDNA, mRNA sequence.

BE841809

BE841809.1 GI:10274187

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 339)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-MR1-SN0065-220

500-006-d05&t3=2000-05-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 62

High quality sequence stop: 338.

Location/Qualifiers

1..339

/organism="Homo sapiens"

FEATURES

source

1..339

RESULT 33

BF410784/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BF410784 333 bp mRNA linear EST 28-NOV-2000

UI-R-CN0-bml-a-02-0-UI-s1 UI-R-CN0 Rattus norvegicus cDNA clone

UI-R-CN0-bml-a-02-0-UI 3', mRNA sequence.

BF410784

BF410784.1 GI:11398759

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 333)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

normalized bladder library cDNA Library Preparation: M.B. Soares

Lab Clone distribution: clones will be available through Research

Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1..333

FEATURES

source

1..333

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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0065"
/note="Organ: stomach normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 339;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
    |||||
Db 57 GCAGTCATGGAGATGGCT 76

RESULT 35
CR477607/c
LOCUS      CR477607 Rat pBluescript Lion Rattus norvegicus cDNA clone
DEFINITION LIONp463H12407 3', mRNA sequence.
ACCESSION  CR477607
VERSION     CR477607.1 GI:49905109
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (Bases 1 to 344)
Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueter, T.,
Schuette, D., Wendel, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Rat ArrayTAG cDNA
Unpublished (2004)
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: LIONp463H12407.
RZPDLIB;
Rat ArrayTAG cDNA
http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=463 Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACACAGCTATGAC.

FEATURES
    source
        Location/Qualifiers
            1..344
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /clone="LIONp463H12407"
                /lab_host="DH10B"
                /clone_lib="Rat pBluescript Lion"

ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 344;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20

```

```

Db 282 GCAGTAGATGGAGAGTGGCT 263
    |||||
RESULT 36
BF849242
LOCUS      BF849242
DEFINITION CM3-EN0079-111100-474-el2 EN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF849242
VERSION     BF849242.1 GI:12236392
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (Bases 1 to 361)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0079-
111100-474-el2&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 343.
Location/Qualifiers
    1..361
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="Adult"
        /clone_lib="EN0079"
        /note="Organ: lung normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      84.0%; Score 16.8; DB 2; Length 361;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
    |||||
Db 121 GCTGTTAATGGAGAGTGGCT 140

RESULT 37
BF521948
LOCUS      BF521948
DEFINITION UI-R-Y0-aca-a-06-0-UI.r1 UI-R-Y0 Rattus norvegicus cDNA clone
ACCESSION  BF521948
KEYWORDS    UI-R-Y0-aca-a-06-0-UI 5', mRNA sequence.

ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 344;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20

```

```

VERSION      BF521948.1  GI:11629915
KEYWORDS     EST.
SOURCE       Rattus norvegicus (Norway rat)
ORGANISM     Rattus norvegicus
REFERENCE    1 (bases 1 to 372)
AUTHORS      Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE        Normalization and subtraction: two approaches to facilitate gene
JOURNAL      Genome Res. 6 (9), 791-806 (1996)
MEDLINE      97044477
PUBMED       8889548
COMMENT      Contact: Soares, MB
              Coordinated Laboratory for Computational Genomics
              University of Iowa
              375 Newton Road., 4156 MEERF, Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: bento-soares@uiowa.edu
              cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
              clones will be available through Research Genetics (www.resgen.com)
              This clone is also available through the I.M.A.G.E. Consortium at
              LLNL (info@image.llnl.gov). IMAGE ID= 1791356
              Seq primer: M13 Forward.
              Location/Qualifiers
                1..372
                  /organism="Rattus norvegicus"
                  /mol_type="mRNA"
                  /strain="Sprague-Dawley"
                  /db_xref="taxon:10116"
                  /clones="UI-R-Y0-aca-a-06-0-UI"
                  /dev_stages="adult"
                  /clone_libs="UI-R-Y0"
                  /note="Vector: p7773D-Pac (Pharmacia) with a modified
                    polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0
                    library is a subtracted library derived from an
                    individually-tagged normalized whole-eye (minus the lens)
                    library. The driver for the subtraction consisted of a
                    pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
                    UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
                    3-5 nucleotides present between the Not I site and the
                    oligo-AT track which allows identification of the library
                    of origin of a clone within the mixture. The subtracted
                    library (UI-R-Y0) was constructed as follows: PCR
                    amplified cDNA inserts from previous library clones from
                    which 3' ESTs had been derived were used as a driver in a
                    hybridization with the normalized whole-eye library in
                    the form of single-stranded circles. The remaining
                    single-stranded circles (subtracted library) was purified
                    by hydroxyapatite column chromatography, converted to
                    double-stranded circles and electroporated into DH10B
                    bacteria (Life Technologies) to generate the UI-R-Y0
                    library. This procedure has been previously described
                    (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                    1996)"

FEATURES             source
  source
    1..374
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2549831"
      /tissue_type="normal epithelium"
      /lab_host="DH10B"
      /clone_lib="NCI_CGAP_Ov38"
      /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
        Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
        Library constructed by Life Technologies."

ORIGIN
Query Match      84.0%; Score 16.8; DB 1; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
        |||||
        358 GCTGTATATGGAGAGTGGCT 339

Db

RESULT 39
H37761/c
LOCUS
DEFINITION
YD46C03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190468 3', mRNA sequence.
H37761
H37761.1  GI:907260
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mafrà,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  
```

Email: est@watson.wustl.edu

Insert Size: 3093

High quality sequence stops: 348

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 3093 Std Error: 0.00

Seq primer: Promega -21mi3

High quality sequence stop: 348.

Location/Qualifiers

1..379

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3846877"

/db_xref="taxon:9606"

/clone="IMAGE:130468"

/sex="male"

/tissue_type="retina"

/dev_stage="55 year old"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Scares retina Nzb4HR"

/note="Organ: eye; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAACTGAAGTCGAGCGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 379;

Best Local Similarity 90.0%; Pred.No.1.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGCAGAGTGCC 20
||| ||||||||| |||

Db 172 GCTGTTAATGCAGAGTGCC 153

RESULT 40

W42610

LOCUS

DEFINITION

wc3rd08.r1 Soares_senescent_fibroblasts_NbH3F Homo sapiens CDNA clone IMAGE:323151 5', mRNA sequence.

W42610

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rehlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson.R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

```

/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-Y0"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-B0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)"

```

ORIGIN

```

Query Match      84.0%; Score 16.8; DB 2; Length 390;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GCAGTTATGAGAGTGGCT 20
||||| ||||| ||||| ||||| |||||
Db 277 GCAGTAGTAGGAGAGTGGCT 296

```

```

RESULT 42
N33486/c
LOCUS      393 bp mRNA linear EST 10-JAN-1996
DEFINITION Y42f09.sl Soares melanocyte 2Nohm Homo sapiens cDNA clone
IMAGE:273929 3', mRNA sequence.
ACCESSION  N33486
VERSION    N33486.1 GI:1153885
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

```

```

REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaekis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 261
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 261.

```

FEATURES

```

source
1..393
Location/Qualifiers

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3883571"

```

```

/db_xref="taxon:9606"
/clone="IMAGE:273929"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2Nohm"
/notes="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTCGAGCGCGCAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

```

ORIGIN

```

Query Match      84.0%; Score 16.8; DB 7; Length 393;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GCAGTTATGAGAGTGGCT 20
||||| ||||| ||||| ||||| |||||
Db 171 GCTGTTAATGAGAGTGGCT 152

```

```

RESULT 43
AI559323/c
LOCUS      410 bp mRNA linear EST 13-MAY-1999
DEFINITION tq43f08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211591 3',
mRNA sequence.
ACCESSION  AI559323
VERSION    AI559323.1 GI:4509528
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

```

```

REFERENCE
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 2770 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 406
POLYA=No.

```

FEATURES

```

source
1..410
Location/Qualifiers

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2211591"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

```

ORIGIN

```

Query Match      84.0%; Score 16.8; DB 1; Length 410;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
DB      186 GCTGTTAATGGAGAGTGGCT 167

RESULT 44
W42606/CL
LOCUS      W42606              413 bp      mRNA      linear      EST 21-MAY-1996
DEFINITION clone IMAGE:323151 3', mRNA sequence.
ACCESSION  W42606
VERSION    W42606.1  GI:1327036
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 413)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,L., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
            Wilson,R.
TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Willson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 391.

FEATURES             Location/Qualifiers
     source            1..413
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1254663"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:323151"
                     /tissue_type="senescent fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_senescent_fibroblasts_NHSP"
                     /note="vector: pTV73D (Pharmacia) with a modified
                     polylinker V.TYPE: phagemid; Site 1: Not I; Site 2: Eco
                     RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5',
                     TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pTV73 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo."

ORIGIN

Query Match      84.0%; Score 16.8; DB 7; Length 413;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAGTTAATGGAGAGTGGCT 20
DB      172 GCTGTTAATGGAGAGTGGCT 153

RESULT 45

```

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1665

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1665 Std Error: 0.00

Seq primer: Promega -21m13

High quality sequence stop: 349.

Location/Qualifiers

FEATURES

source

1. .417

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:413372"

/db_xref="taxon:9606"

/clone="IMAGE:40831"

/sex="female"

/dev stages="73 days post natal"

/lab host="DH10B (ampicillin resistant)"

/clone_lib="Soares infant brain INIB"

/note="Organ: whole brain; Vector: Lefmid BA; Site 1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dT) primer [5,

AACTGGAGAAATCGCGCCGAGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lefmid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 417;

Best Local Similarity 90.0%; Pred. No. 1.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20

DB 181 GCTGTATGGAGAGTGCT 162

RESULT 47

CN388155

DEFINITION 17000531328114 GRN_EB Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004

ACCESSION CN388155

KEYWORDS CN388155.1 GI:47375750

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 418)

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

Lebkowski, J and Stanton, L.W

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 418 Std Error: 0.00.

Location/Qualifiers

FEATURES

source

1. .418

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, embryoid bodies

derived from H1, H7 and H9 cells"

/clone_lib="GRN_EB"

/note="oligo dT primed, full-length enriched cDNA library

from embryoid body outgrowths derived from HES cell lines

H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free

conditions."

ORIGIN

Query Match 84.0%; Score 16.8; DB 7; Length 418;

Best Local Similarity 90.0%; Pred. No. 1.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20

DB 164 GCAGTCATGGAGATGGCT 183

RESULT 48

CN100560

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Features

Source

1. .431

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/strain="T89"

/db_xref="taxon:47664"

/clone="C050P42"

/tissue_type="leaf"

/clone_lib="Populus strain T89 leaves"

1. .431

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/strain="T89"

/db_xref="taxon:47664"

/clone="C050P42"

/tissue_type="leaf"

/clone_lib="Populus strain T89 leaves"

1. .431

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/strain="T89"

/db_xref="taxon:47664"

/clone="C050P42"

/tissue_type="leaf"

/clone_lib="Populus strain T89 leaves"

1. .431

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/strain="T89"

/db_xref="taxon:47664"

/clone="C050P42"

/tissue_type="leaf"

/clone_lib="Populus strain T89 leaves"

1. .431

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/strain="T89"

/db_xref="taxon:47664"

/clone="C050P42"

/tissue_type="leaf"

/clone_lib="Populus strain T89 leaves"

1. .431

/organism="Populus tremula x Populus tremuloides"

AA350346
 VERSION AA350346.1 GI:2002737
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 432)
 AUTHORS Adams M.D., Kerlavage A.R., Fields C. and Venter J.C.
 TITLE 3,400 expressed sequence tags identify diversity of transcripts from human brain
 JOURNAL Nat. Genet. 4, 256-267 (1993)
 MEDLINE 93364420
 PUBMED 8358434
 COMMENT Other ESTs: EST57668 THCI:92694
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 Location/Qualifiers
 1..432
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):151132"
 /db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Infant brain"
 /clone_lib="Infant brain"
 /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI"

ORIGIN
 Query Match 84.0%; Score 16.8; DB 1; Length 432;
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 DB 193 GCAGTCAATGGAGAGTGGCT 212

RESULT 50
 AA36245/c
 LOCUS AA36245.1
 DEFINITION zv24902.s1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:754610
 3', mRNA sequence.
 ACCESSION AA36245
 VERSION AA36245.1 GI:2141159
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 440)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Scheillenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m13 fwd. ET from Amersham
 High quality sequence stop: 367.

FEATURES
 source
 Location/Qualifiers
 1..440
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5977520"
 /db_xref="taxon:9606"
 /clone="IMAGE:754610"
 /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares NHMPu_S1"
 /note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbM, pregnant uterus NbHEU, and fetal heart NbHH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN
 Query Match 84.0%; Score 16.8; DB 1; Length 440;
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 DB 176 GCTGTAAATGGAGAGTGGCT 157

Search completed: December 3, 2004, 05:49:40
 Job time : 2609.05 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 20:35:25 ; Search time 265.789 Seconds
(without alignments)

367.363 Million cell updates/sec

Title: US-10-050-189A-8

Perfect score: 20

Sequence: 1 gcagtttaatggagagtggtc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_23Sep04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	ABN84786
2	20	100.0	66479	6	ABQ80567
3	20	100.0	66479	6	ABQ80566
4	20	100.0	66479	6	ABQ80568
5	20	100.0	66479	6	ABQ80565
6	17.4	87.0	22791	4	AAK69857
7	16.8	84.0	589	6	ABV98005
8	16.8	84.0	2637	4	AAK94484
9	16.8	84.0	2637	12	ADL31281
10	16.8	84.0	2878	2	AAZ77516
11	16.8	84.0	4071	5	AAK83893
12	16.8	84.0	4977	6	ABL61892
13	16.8	84.0	4977	6	ABK84229
14	16.8	84.0	4977	12	ADL83261
15	16.8	84.0	5115	10	ADF28873
16	16.8	84.0	5157	3	AAZ77462
17	16.8	84.0	5178	2	AAK35732
18	16.8	84.0	5457	2	AAK35733
19	16.8	84.0	5642	8	ABX62937
20	16.8	84.0	5768	5	AAK65659
21	16.8	84.0	5828	10	ADE25701

C	22	16.8	84.0	6092	5	AAS65021	Aas65021 DNA encod
	23	16.8	84.0	6291	5	AAS66214	Aas66214 DNA encod
	24	16.8	84.0	8426	8	ACC72047	ACC72047 BCU0586 g
	25	16.8	84.0	8490	6	ABQ79531	Abq79531 Human FN1
	26	16.8	84.0	28220	4	AAS27653	Aas27653 DNA encod
	27	16.8	84.0	28220	4	AAS27652	Aas27652 DNA encod
C	28	16.8	84.0	29220	10	ADB94455	Adb94455 Novel hum
	29	16.8	84.0	29220	10	ADB94456	Adb94456 Novel hum
	30	16.8	84.0	68940	2	AAK57351	Aak57351 Human chr
	31	16.8	84.0	110000	4	AAK95240_04	Continuation (5 of
	32	16.8	84.0	110000	4	AAK95240_08	Continuation (9 of
	33	16.8	84.0	110000	4	AAK95733_04	Continuation (5 of
	34	16.8	84.0	110000	4	AAK95733_08	Continuation (9 of
	35	16.8	84.0	110000	6	ABT00010_04	Continuation (5 of
	36	16.8	84.0	110000	6	ABT00010_08	Continuation (9 of
	37	16.8	84.0	110000	6	ABT01503_04	Continuation (5 of
	38	16.8	84.0	110000	6	ABT01503_08	Continuation (9 of
	39	16.8	84.0	110000	12	ADH77482_04	Continuation (5 of
	40	16.8	84.0	110000	12	ADH77482_08	Continuation (9 of
	41	16.8	84.0	158811	12	ADH77486_08	Adh77486 Human sof
	42	16.4	82.0	52216	4	AAH28355	Aah28355 Nucleotid
	43	16.4	82.0	52216	6	ABL50307	Ab150307 Human mus
	44	16.4	80.0	29	4	AAI70577	Aai70577 Human ser
	45	16.8	80.0	509	3	AAK59296	Aas59296 C-termina
	46	16.8	80.0	1336	4	AAI70575	Aai70575 Human ser
	47	16.8	80.0	1770	5	AAI14461	Aad14461 Human pyr
	48	16.8	80.0	1770	10	ADD22938	Ad22938 CDNA enco
	49	16.8	80.0	2477	4	AAH16282	Aah16282 Human cdn
	50	16.8	80.0	2477	12	ADN04811	Adn04811 Antipsori
	51	16.8	80.0	2477	12	ADN04811	Adn04811 Antipsori
	52	16.8	80.0	2477	12	ADO20209	Ado20209 Human PRO
	53	16.8	80.0	2674	4	AAI65020	Aai65020 Serine/th
	54	16.8	80.0	12460	6	ABL32069	Ab132069 Human imm
	55	16.8	80.0	20892	5	ABA15709	Abai5709 Human ner
	56	15.8	79.0	318	9	ADA28734	Ada28734 DNA encod
	57	15.8	79.0	780	4	AAH06120	Aah06120 Human CDN
	58	15.8	79.0	780	4	AAH06120	Aah06120 Human CDN
	59	15.8	79.0	896	6	ABT03409	Abt03409 Ovary cel
	60	15.8	79.0	998	6	ABT03410	Abt03410 Ovary cel
	61	15.8	79.0	1830	8	ACA54254	Acas4254 Prokaryot
	62	15.8	79.0	2369	2	AAV38669	Aav38669 Mus muscu
	63	15.8	79.0	4335	2	AAV69634	Aav69634 TPR motif
	64	15.8	79.0	4931	2	AAV69635	Aav69635 TPR motif
	65	15.8	79.0	5739	10	AAK53964	Aak53964 Mouse KIF
	66	15.8	79.0	6476	2	AAV69636	Aav69636 TPR motif
	67	15.8	79.0	6476	10	ADD15193	Ad15193 Human TPR
	68	15.8	79.0	15676	3	ADL1288	Adl1288 Arabidops
	69	15.8	79.0	17111	3	ADL1289	Adl1289 Arabidops
	70	15.8	79.0	17116	3	ADL1290	Adl1290 Arabidops
	71	15.8	79.0	18820	4	AAK03764	Aak03764 Human rep
	72	15.8	79.0	18820	4	ABA07938	Abao7938 Human ova
	73	15.8	79.0	32191	4	AAI03766	Aai03766 Human rep
	74	15.8	79.0	32191	4	ABA07940	Abao7940 Human ova
	75	15.8	79.0	41239	4	AAK78622	Aak78622 Human imm
	76	15.8	79.0	90583	8	ACD13447	Accl13447 Human DNA
	77	15.8	79.0	110000	12	ADO34927_1	Continuation (2 of
	78	15.4	77.0	56	3	AAA70932	Continuation (2 of
	79	15.4	77.0	56	3	AAA70949	AAA70949 Molecular
	80	15.4	77.0	306	4	AAI25832	Aai25832 Probe #15
	81	15.4	77.0	306	4	ABA72499	Abi72499 Human foe
	82	15.4	77.0	306	4	AAI52911	Aai52911 Probe #21
	83	15.4	77.0	306	4	ABA38257	Abi38257 Probe #16
	84	15.4	77.0	306	4	AAK47075	Aak47075 Human bon
	85	15.4	77.0	306	4	AAK20923	Aak20923 Human bra
	86	15.4	77.0	306	4	ABA46836	Abi46836 Human liv
	87	15.4	77.0	306	6	ABS21310	Abi21310 Human gen
	88	15.4	77.0	464	4	AAK32922	Aak32922 Probe #79
	89	15.4	77.0	464	4	AAK33531	Aak33531 Human bon
	90	15.4	77.0	464	4	AAK077005	Aak077005 Human bra
	91	15.4	77.0	464	4	ABS33300	Abi33300 Human liv
	92	15.4	77.0	464	6	ABS08383	Abi08383 Human gen
	93	15.4	77.0	589	4	AAI16636	Aai16636 Probe #65
	94	15.4	77.0	589	4	ABA59958	Abi59958 Human foe

C 95	15.4	77.0	589	4	AAI39830	Probe #85	168	15.2	76.0	3042	6	ABV78118	Human eph
C 96	15.4	77.0	589	4	ABA28378	Probe #68	169	15.2	76.0	3042	6	ABZ35694	Human eph
C 97	15.4	77.0	589	4	AAK34107	Human bron	170	15.2	76.0	3042	6	ABX09937	Human eph
C 98	15.4	77.0	589	4	AAK08229	Human bron	171	15.2	76.0	3042	6	ABL91659	Human pol
C 99	15.4	77.0	589	4	ABS33906	Human liv	172	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 100	15.4	77.0	589	6	ABS08876	Human gen	173	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 101	15.4	77.0	873	8	ACA40140	Prokaryot	174	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 102	15.4	77.0	1118	12	ADN41558	Novel hum	175	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 103	15.4	77.0	1122	2	AXX27338	Human sec	176	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 104	15.4	77.0	1122	9	ADA07217	Human CDN	177	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 105	15.4	77.0	1122	12	ADNA0897	Novel hum	178	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 106	15.4	77.0	5044	6	AAI38609	Genomic D	179	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 107	15.4	77.0	6819	4	ABL26375	Drosophil	180	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 108	15.4	77.0	7151	6	AAI70693	Alfalfa a	181	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 109	15.4	77.0	7175	8	ABX13439	M. sativa	182	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 110	15.4	77.0	9444	4	ABL26374	Drosophil	183	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 111	15.4	77.0	32176	4	AAI05628	Human rep	184	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 112	15.4	77.0	32250	4	AAI05627	Human rep	185	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 113	15.4	77.0	65237	6	ABA90193	Continuation (5 of	186	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 114	15.4	77.0	65237	6	ABQ87681	Continuation (5 of	187	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 115	15.4	77.0	65237	6	ABX33717	Continuation (5 of	188	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 116	15.4	77.0	92000	10	ADB8139T	Continuation (4 of	189	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 117	15.4	77.0	99916	6	ADIO3931	Human enz	190	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 118	15.2	76.0	35	2	AXX05509	Synthetic	191	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 119	15.2	76.0	35	6	ABL94485	Fibronect	192	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 120	15.2	76.0	35	12	ADI32396	Adi32396 Oligo pri	193	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 121	15.2	76.0	300	2	AXX05527	Aax05527 Fibronect	194	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 122	15.2	76.0	300	12	ADL32486	Adi32486 Human fib	195	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 123	15.2	76.0	308	6	ABL94503	Mutant fi	196	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 124	15.2	76.0	308	10	ADZ39208	Adz39208 Human fib	197	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 125	15.2	76.0	308	10	ABX13975	Abx13975 DNA encod	198	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 126	15.2	76.0	330	5	AA564309	Aas64309 DNA encod	199	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 127	15.2	76.0	387	5	ACH66513	Aaf66513 Novel hum	200	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 128	15.2	76.0	412	9	ACH46313	Ach46313 Human inf	201	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 129	15.2	76.0	416	9	ACH17364	Ach17364 Human adu	202	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 130	15.2	76.0	458	3	AC43573	Zea may	203	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 131	15.2	76.0	573	3	ABN63733	Abn63733 Human can	204	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 132	15.2	76.0	618	10	ADE39211	Ade39211 Human FNF	205	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 133	15.2	76.0	663	10	ADE39211	Ade39211 Human FNF	206	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 134	15.2	76.0	684	10	ADE39213	Ade39213 Human FNF	207	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 135	15.2	76.0	687	10	ADE39217	Ade39217 Human FNF	208	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 136	15.2	76.0	704	10	ADE39215	Ade39215 Human FNF	209	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 137	15.2	76.0	765	10	ACF66849	Acf66849 Phototrab	210	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 138	15.2	76.0	767	10	ACF66549	Acf66549 Phototrab	211	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 139	15.2	76.0	994	3	AAH43486	Aah43486 Zea may	212	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 140	15.2	76.0	994	4	AAH32565	Aah32565 Human sec	213	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 141	15.2	76.0	1002	5	AAH42034	Aah42034 Follicula	214	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 142	15.2	76.0	1050	4	AAH99494	Aah99494 Human EST	215	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 143	15.2	76.0	1142	3	AC67673	Ac67673 Human sec	216	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 144	15.2	76.0	1170	2	AAAT67137	Aat67137 Coprinus	217	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 145	15.2	76.0	1275	10	ACF71771	Acf71771 Phototrab	218	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 146	15.2	76.0	1305	11	ACH98708	Ach98708 Klebsiell	219	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 147	15.2	76.0	1332	11	ACH98103	Ach98103 Klebsiell	220	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 148	15.2	76.0	1431	4	ABL19535	Ab119535 Drosophil	221	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 149	15.2	76.0	1479	4	AAH99421	Aah99421 Human EST	222	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 150	15.2	76.0	1545	4	AAH99421	Aah99421 Human sec	223	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 151	15.2	76.0	1600	3	AAH99421	Aah99421 Human sec	224	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 152	15.2	76.0	1743	8	ABX75865	Abx75865 Rat Neur-	225	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 153	15.2	76.0	1809	8	ACA53739	Acas3739 Prokaryot	226	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 154	15.2	76.0	1858	10	ADBS58725	Adbs58725 Toxicity	227	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 155	15.2	76.0	1858	10	ADBS53420	Adbs53420 Primary r	228	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 156	15.2	76.0	1859	4	AAH32527	Aah32527 Human sec	229	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 157	15.2	76.0	1865	6	ABQ77562	Abq77562 Human ova	230	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 158	15.2	76.0	1978	8	ABQ77562	Abq77562 Human ova	231	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 159	15.2	76.0	2349	8	ABZ82148	Abz82148 Cowpea 9-	232	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 160	15.2	76.0	2392	10	AD121932	Ad121932 Novel hum	233	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 161	15.2	76.0	2480	10	ADA20684	Ada20684 Rice CDNA	234	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 162	15.2	76.0	2581	6	ABN87815	Abn87815 Human ova	235	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 163	15.2	76.0	2581	8	ABX92241	Abx92241 Human ova	236	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 164	15.2	76.0	2590	6	ABZ11889	Abz11889 Human pol	237	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 165	15.2	76.0	2590	12	ADMA4407	Adma4407 Novel hum	238	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 166	15.2	76.0	2613	4	AAH15201	Aah15201 Human CDN	239	15.2	76.0	3042	6	ABZ77317	Nucleotid
C 167	15.2	76.0	2743	8	ABZ77319	Abz77319 Nucleotid	240	15.2	76.0	3042	6	ABZ77317	Nucleotid

241	14.8	74.0	953	12	ADJ39949	Adj39949 Plant cDN	8	ACA91046	Novel hum
242	14.8	74.0	987	8	ACA47128	Prokaryot	8	ACA70828	Human sec
243	14.8	74.0	1045	3	AAC44329	AAC44329 Arabidops	8	ACA95338	Novel hum
244	14.8	74.0	1131	10	ACC61133	Acc61133 Gene sequ	8	ACC86281	Human sec
245	14.8	74.0	1131	10	ADK62291	Adk62291 Disease t	8	ACC90153	Human sec
246	14.8	74.0	1182	5	AHA65561	Aha65561 C glutami	8	ACD12761	Human sec
247	14.8	74.0	1182	8	ACA00018	AcA00018 C. Glutam	8	ACF19991	Human sec
248	14.8	74.0	1216	3	AAC50206	Aac50206 Arabidops	8	ABX76935	Human PRO
249	14.8	74.0	1220	3	AAC39770	Aac39770 Arabidops	8	ACA73267	Novel hum
250	14.8	74.0	1243	3	AAC40472	Aac40472 Arabidops	8	ACA68810	Novel hum
251	14.8	74.0	1467	12	ADI43304	Adi43304 plant tra	8	ACA74654	CDNA enco
252	14.8	74.0	1551	5	ABV24558	Abv24558 Human pro	8	ACA70521	Human sec
253	14.8	74.0	1734	2	AAX23748	Aax23748 Rice anth	8	ACD14707	Human PRO
254	14.8	74.0	1734	2	AAX23754	Aax23754 Rice anth	8	ACD14707	Human PRO
255	14.8	74.0	1785	8	ADA69857	Ada69857 Rice gene	8	ACA68379	Novel hum
256	14.8	74.0	1815	10	ADH83966	Adh83966 Enterococ	8	ABX98844	Novel hum
257	14.8	74.0	1822	6	ABL56595	AbL56595 Nucleotid	8	ACC81321	Human sec
258	14.8	74.0	1893	6	ABN67234	Abn67234 Streptoco	8	ACA95645	Novel hum
259	14.8	74.0	2085	4	AD07973	Ad07973 Corn cyst	8	ACC80004	Human sec
260	14.8	74.0	2085	10	ADF70675	Adf70675 Corn cyst	8	ACF12666	Human sec
261	14.8	74.0	2238	5	AAS67180	Aas67180 DNA enco	8	ACA65155	Human PRO
262	14.8	74.0	2239	5	AAS83892	Aas83892 DNA enco	8	ACA65155	Human PRO
263	14.8	74.0	2324	6	ABK71536	Abk71536 Human dit	8	ACA73881	Human sec
264	14.8	74.0	2324	3	AAA37136	Aaa37136 Human PRO	8	ACA74293	Novel hum
265	14.8	74.0	2340	4	AAFA5479	Aaf54479 Primer #1	8	ACA96688	Human PRO
266	14.8	74.0	2340	4	AAS46114	Aas46114 Human DNA	8	ACD10794	CDNA enco
267	14.8	74.0	2340	8	ACA89564	AcA89564 CDNA enco	8	ACC91490	Human sec
268	14.8	74.0	2340	8	ACA73574	AcA73574 Human sec	8	ACD02825	CDNA enco
269	14.8	74.0	2340	8	ACA05889	AcA05889 Human sec	8	ACC87390	Human sec
270	14.8	74.0	2340	8	ACA66723	AcA66723 cDNA enco	8	ACC87390	Human sec
271	14.8	74.0	2340	8	ACF20298	AcF20298 Human sec	8	ACA54562	Human PRO
272	14.8	74.0	2340	8	ACF19684	AcF19684 Human sec	8	ACA94279	Human sec
273	14.8	74.0	2340	8	ACD21972	AcD21972 Human sec	8	ACA98023	Human PRO
274	14.8	74.0	2340	8	ACF13137	AcF13137 Human sec	8	ACA91525	Novel hum
275	14.8	74.0	2340	8	ACD25240	AcD25240 Human sec	8	ACA90739	Novel hum
276	14.8	74.0	2340	8	ACF00289	AcF00289 Human sec	8	ACD16286	Human sec
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C 635 14.8 74.0 2340 9 ACF51702 Human sec
C 636 14.8 74.0 2340 9 ACF33625 Human sec
C 637 14.8 74.0 2340 9 ACD49878 Human sec
C 638 14.8 74.0 2340 9 ACF37660 Human sec
C 639 14.8 74.0 2340 9 ACF28645 Human sec
C 640 14.8 74.0 2340 9 ACD88721 Human sec
C 641 14.8 74.0 2340 9 ACF75340 Human sec
C 642 14.8 74.0 2340 9 ACF61161 Human sec
C 643 14.8 74.0 2340 9 ACF44317 Human sec
C 644 14.8 74.0 2340 9 ACH08559 Human sec
C 645 14.8 74.0 2340 9 ACC93946 Human sec
C 646 14.8 74.0 2340 9 ACD21051 Human sec
C 647 14.8 74.0 2340 9 ACF06833 Human sec
C 648 14.8 74.0 2340 9 ACD20744 Human sec
C 649 14.8 74.0 2340 9 ACD22893 Human sec
C 650 14.8 74.0 2340 9 ACF41593 Human sec
C 651 14.8 74.0 2340 9 ACF07140 Human sec
C 652 14.8 74.0 2340 9 ACF77796 Human sec
C 653 14.8 74.0 2340 9 ACD46194 Human sec
C 654 14.8 74.0 2340 9 ACF47097 Human sec
C 655 14.8 74.0 2340 9 ACF54465 Human sec
C 656 14.8 74.0 2340 9 ACF45869 Human sec
C 657 14.8 74.0 2340 9 ACF45562 Human sec
C 658 14.8 74.0 2340 9 ACF38581 Human sec
C 659 14.8 74.0 2340 9 ACD89642 Human sec
C 660 14.8 74.0 2340 9 ACD85344 Human sec
C 661 14.8 74.0 2340 9 ACD85958 Human sec
C 662 14.8 74.0 2340 9 ACF75954 Human sec
C 663 14.8 74.0 2340 9 ACF60854 Human sec
C 664 14.8 74.0 2340 9 ACH05741 cDNA enco
C 665 14.8 74.0 2340 9 ADA82814 Human sec
C 666 14.8 74.0 2340 9 ACF56000 Human sec
C 667 14.8 74.0 2340 10 ACF55386 Human sec
C 668 14.8 74.0 2340 10 ADB86122 Human sec
C 669 14.8 74.0 2340 10 ACF56307 Human sec
C 670 14.8 74.0 2340 10 ACF58614 Human sec
C 671 14.8 74.0 2340 10 ACF55693 Human sec
C 672 14.8 74.0 2340 10 ACF55079 Human sec
C 673 14.8 74.0 2340 10 ACD18263 Human PRO
C 674 14.8 74.0 2340 10 ADD05852 Human sec
C 675 14.8 74.0 2340 10 ADD70909 Human CDN
C 676 14.8 74.0 2340 10 ADD39986 Human CDN
C 677 14.8 74.0 2340 10 ADD70432 Human CDN
C 678 14.8 74.0 2340 10 ADD38553 Human CDN

C 679	14.8	74.0	2340	10	ADD39509	Human	CDN	752	14.8	74.0	3349	3	AAA88549	Aaa88549 Human CAS
C 680	14.8	74.0	2340	10	ADD39032	Human	CDN	753	14.8	74.0	3349	8	ABX12548	Abx12548 CDNA enco
C 681	14.8	74.0	2340	10	ADD40463	Human	CDN	754	14.8	74.0	3349	12	ADL61078	Adl61078 Human pro
C 682	14.8	74.0	2340	10	ADE50684	Human	CDN	755	14.8	74.0	4049	2	AAQ90660	Aaq90660 Eph-relat
C 683	14.8	74.0	2340	10	ADE50296	Human	CDN	756	14.8	74.0	4097	2	AAQ90657	Aaq90657 Eph-relat
C 684	14.8	74.0	2340	10	ADE50207	Human	CDN	757	14.8	74.0	4569	12	ADO29747	Ado29747 Human nov
C 685	14.8	74.0	2340	10	ADE21765	Human	CDN	758	14.8	74.0	4698	6	AD27621	Ad27621 Human col
C 686	14.8	74.0	2340	10	ADF30190	Human	CDN	759	14.8	74.0	4711	12	ADO28626	Ado28626 Human EPH
C 687	14.8	74.0	2340	10	ADF56083	Human	CDN	760	14.8	74.0	5218	8	AB242778	Ab242778 Human bra
C 688	14.8	74.0	2340	10	ADG02847	Novel	hum	761	14.8	74.0	5252	10	ADI02477	Adi02477 Human CDN
C 689	14.8	74.0	2340	10	ADG01554	Novel	hum	762	14.8	74.0	5267	2	AAx211357	Aax211357 Human BAI
C 690	14.8	74.0	2340	10	ADF95729	Novel	hum	763	14.8	74.0	5749	2	AAz28003	Aaz28003 Nucleotid
C 691	14.8	74.0	2340	10	ADG12544	Novel	hum	764	14.8	74.0	5749	3	AAA96030	Aaa96030 Human lec
C 692	14.8	74.0	2340	10	ADH09204	Human	PRO	765	14.8	74.0	5749	6	ABK94720	Abk94720 Neurodege
C 693	14.8	74.0	2340	10	ADH98587	Human	CDN	766	14.8	74.0	5948	3	AAg93101	Aag93101 Human sec
C 694	14.8	74.0	2340	10	ABX78717	Human	PRO	767	14.8	74.0	6057	8	AB234857	Ab234857 Coding se
C 695	14.8	74.0	2340	10	ACA75689	Novel	hum	768	14.8	74.0	6057	11	ADN39658	Adn39658 Cancer/an
C 696	14.8	74.0	2340	10	ACA71169	Human	sec	C 769	14.8	74.0	6260	4	ABL19904	Ab119904 Drosophil
C 697	14.8	74.0	2340	10	ACC87697	Human	sec	C 770	14.8	74.0	6287	4	ABL28794	Ab128794 Drosophil
C 698	14.8	74.0	2340	10	ACC87083	Human	sec	C 771	14.8	74.0	8077	6	ABN80165	Abn80165 Human che
C 699	14.8	74.0	2340	10	ACD04256	Human	sec	C 772	14.8	74.0	8989	4	AA805297	Aas05297 Pig alpha
C 700	14.8	74.0	2340	10	ACA69587	CDNA	enco	C 773	14.8	74.0	11470	4	AA411754	Aas411754 Genomic s
C 701	14.8	74.0	2340	10	ACA90432	Novel	hum	C 774	14.8	74.0	15424	4	AB127214	Ab127214 Drosophil
C 702	14.8	74.0	2340	10	ACC89539	Human	sec	C 775	14.8	74.0	16335	4	ABL25211	Ab125211 Drosophil
C 703	14.8	74.0	2340	10	ACA98330	Novel	hum	C 776	14.8	74.0	18603	4	ABL25210	Ab125210 Drosophil
C 704	14.8	74.0	2340	10	ACA93972	Human	sec	C 777	14.8	74.0	18831	2	AAV81945	Aav81945 S. putref
C 705	14.8	74.0	2340	10	ACD15365	Human	sec	C 778	14.8	74.0	34446	2	AAx24332	Aax24332 Bovine ad
C 706	14.8	74.0	2340	10	ACD08952	Human	sec	C 779	14.8	74.0	34446	6	ABA92463	Abag92463 Bovine ad
C 707	14.8	74.0	2340	10	ACC96872	Human	sec	C 780	14.8	74.0	34446	6	ABA97532	Abag97532 Bovine ad
C 708	14.8	74.0	2340	10	ACF15593	Human	sec	C 781	14.8	74.0	37895	2	AA734137	Aat34137 Gene for
C 709	14.8	74.0	2340	10	ACA29660	Human	PRO	C 782	14.8	74.0	37895	2	AAV00503	Aav00503 S. putref
C 710	14.8	74.0	2340	10	ACD03132	Novel	hum	C 783	14.8	74.0	37895	3	AAH71518	Aah71518 Shewanell
C 711	14.8	74.0	2340	10	ACD01947	Novel	hum	C 784	14.8	74.0	37895	4	AAH47833	Aah47833 S. putref
C 712	14.8	74.0	2340	10	ACA92139	Novel	hum	C 785	14.8	74.0	37913	2	AAQ51128	Aaq51128 Eicosapen
C 713	14.8	74.0	2340	11	ADL32985	Human	CDN	C 786	14.8	74.0	53226	10	ABQ76896	Abq76896 Human G-P
C 714	14.8	74.0	2340	11	ADM30519	Novel	hum	C 787	14.8	74.0	55996	9	ADA02741	Ada02741 Mouse Tnf
C 715	14.8	74.0	2340	12	AD574516	Human	sec	C 788	14.8	74.0	55996	10	ADB72479	Adb72479 Mouse Tnf
C 716	14.8	74.0	2340	12	AD575128	Human	sec	C 789	14.8	74.0	55996	10	ADC85221	Adc85221 Mouse Tnf
C 717	14.8	74.0	2340	12	AD596767	Human	CDN	C 790	14.8	74.0	55996	12	ADM74336	Adm74336 Murine ca
C 718	14.8	74.0	2340	12	AD574516	Human	sec	C 791	14.8	74.0	64976	2	AAV21209_16	AAV21209_16
C 719	14.8	74.0	2340	12	AD574516	Human	sec	C 792	14.8	74.0	70000	6	AD474934	Ad474934 Human pho
C 720	14.8	74.0	2340	12	AD574516	Human	sec	C 793	14.8	74.0	110000	8	AD533224_3	AD533224_3
C 721	14.8	74.0	2340	12	AD574516	Human	sec	C 794	14.8	74.0	110000	8	AD533224_3	AD533224_3
C 722	14.8	74.0	2340	12	AD574516	Human	sec	C 795	14.8	74.0	110000	10	ACF65383_2	ACF65383_2
C 723	14.8	74.0	2340	12	AD574516	Human	sec	C 796	14.8	74.0	110000	10	ACF67367_03	ACF67367_03
C 724	14.8	74.0	2340	12	AD574516	Human	sec	C 797	14.8	74.0	117962	8	AD54480	AD54480 Human CIP
C 725	14.8	74.0	2340	12	AD574516	Human	sec	C 798	14.8	74.0	152048	10	ADL13855	Adl13855 Osteoearth
C 726	14.8	74.0	2340	12	AD574516	Human	sec	C 799	14.8	74.0	349881	10	ADC86642	Adc86642 Human GPC
C 727	14.8	74.0	2340	12	AD574516	Human	sec	C 800	14.8	74.0	349881	5	AAH68525	Aah68525 C glutami
C 728	14.8	74.0	2340	12	AD574516	Human	sec	C 801	14.8	74.0	38	10	ACF80129	ACF80129 Phosphoma
C 729	14.8	74.0	2340	12	AD574516	Human	sec	C 802	14.8	74.0	158	5	AAH81241	Aah81241 Escherich
C 730	14.8	74.0	2340	12	AD574516	Human	sec	C 803	14.8	74.0	158	8	ACA13550	Aca13550 Prokaryot
C 731	14.8	74.0	2340	12	AD574516	Human	sec	C 804	14.8	74.0	178	5	AAH81239	Aah81239 Escherich
C 732	14.8	74.0	2340	12	AD574516	Human	sec	C 805	14.8	74.0	178	5	ACA13563	Aca13563 Prokaryot
C 733	14.8	74.0	2340	12	AD574516	Human	sec	C 806	14.8	74.0	191	5	AAH81240	Aah81240 Escherich
C 734	14.8	74.0	2340	12	AD574516	Human	sec	C 807	14.8	74.0	191	5	ACA13455	Aca13455 Prokaryot
C 735	14.8	74.0	2340	12	AD574516	Human	sec	C 808	14.8	74.0	286	10	ABX87483	Abx87483 Cori ear-
C 736	14.8	74.0	2340	12	AD574516	Human	sec	C 809	14.8	74.0	314	6	ABN18423	Abn18423 Human ORF
C 737	14.8	74.0	2340	12	AD574516	Human	sec	C 810	14.8	74.0	478	4	AAH99875	Aah99875 Human pro
C 738	14.8	74.0	2340	12	AD574516	Human	sec	C 811	14.8	74.0	498	4	ABA43862	Ab43862 Human bre
C 739	14.8	74.0	2340	12	AD574516	Human	sec	C 812	14.8	74.0	498	4	AAK28045	Aak28045 Human bon
C 740	14.8	74.0	2340	12	AD574516	Human	sec	C 813	14.8	74.0	523	12	ACH67035	Ach67035 Human gen
C 741	14.8	74.0	2340	12	AD574516	Human	sec	C 814	14.8	74.0	560	4	ABA60506	Ab60506 Human foe
C 742	14.8	74.0	2340	12	AD574516	Human	sec	C 815	14.8	74.0	560	4	AAI40393	Aai40393 Probe #90
C 743	14.8	74.0	2340	12	AD574516	Human	sec	C 816	14.8	74.0	560	4	AAK34673	Aak34673 Human bon
C 744	14.8	74.0	2340	12	AD574516	Human	sec	C 817	14.8	74.0	560	4	AAK08786	Aak08786 Human bra
C 745	14.8	74.0	2340	12	AD574516	Human	sec	C 818	14.8	74.0	560	4	ABX34445	Abx34445 Human liv
C 746	14.8	74.0	2340	12	AD574516	Human	sec	C 819	14.8	74.0	566	4	AAH10215	Aah10215 Human CDN
C 747	14.8	74.0	2340	12	AD574516	Human	sec	C 820	14.8	74.0	777	4	AAI96022	Aai96022 Human neu
C 748	14.8	74.0	2340	12	AD574516	Human	sec	C 821	14.8	74.0	864	3	AA74582	Aac74582 Human ORF
C 749	14.8	74.0	2340	12	AD574516	Human	sec	C 822	14.8	74.0	908	6	ABN78970	Abn78970 Human ORF
C 750	14.8	74.0	2340	12	AD574516	Human	sec	C 823	14.8	74.0	1064	3	AAF09962	Aaf09962 Fusarium
C 751	14.8	74.0	2340	12	AD574516	Human	sec	C 824	14.8	74.0	1155	6	ABQ69767	Abq69767 Listeria

C 825	14.4	72.0	1176	5	AAH81381	Aah81381 Escherich	C 898	14.2	71.0	203	4	AAH55744	Aah55744 Human bre
C 826	14.4	72.0	1176	6	ABQ67780	Abq67780 Listeria	C 899	14.2	71.0	203	12	ADN40517	Adn40517 Human bre
C 827	14.4	72.0	1176	8	ACA18661	Aca18661 Prokaryot	900	14.2	71.0	211	10	ACD95719	Acd95719 Human col
C 828	14.4	72.0	1386	8	ACA28558	Aca28558 Prokaryot	901	14.2	71.0	234	10	ACD92231	Acd92231 E. faeciu
C 829	14.4	72.0	1456	3	ACA47696	Aca47696 Arabidops	902	14.2	71.0	241	6	ABK38950	Abk38950 cDNA enco
C 830	14.4	72.0	1730	12	ADO62950	Ado62950 Transcrip	903	14.2	71.0	241	8	ACA11279	Aca11279 Human lun
C 831	14.4	72.0	1752	12	ADN73680	Adn73680 Thale cre	904	14.2	71.0	241	8	ACA02465	Aca02465 Lung canc
C 832	14.4	72.0	1834	4	AAH17446	Aah17446 Human cDN	905	14.2	71.0	241	10	ADH46507	Adh46507 Human lun
C 833	14.4	72.0	2235	10	ADB69874	Adb69874 C. neofo	906	14.2	71.0	261	4	AAI29357	Aai29357 Colon tum
C 834	14.4	72.0	2376	10	ADB69513	Adb69513 C. neofo	907	14.2	71.0	261	4	AAI29384	Aai29384 Colon tum
C 835	14.4	72.0	2598	8	ACA27473	Aca27473 Prokaryot	908	14.2	71.0	261	8	ABZ33543	Abz33543 Human col
C 836	14.4	72.0	3452	10	ADF42306	Adf42306 Phosphona	909	14.2	71.0	261	8	ABZ33570	Abz33570 Human col
C 837	14.4	72.0	3775	10	ADB69152	Adb69152 C. neofo	910	14.2	71.0	261	12	ABZ33570	Abz33570 Human col
C 838	14.4	72.0	4021	10	ADBE71233	Adbe71233 Novel hum	911	14.2	71.0	278	12	ADH00540	Adh00540 Kidney di
C 839	14.4	72.0	4035	8	ABT18153	Abt18153 Aspergill	912	14.2	71.0	279	10	ADD31105	Add31105 Rat cDNA
C 840	14.4	72.0	4035	8	ABT19967	Abt19967 Aspergill	913	14.2	71.0	279	10	ADD31105	Add31105 Rat cDNA
C 841	14.4	72.0	4224	4	AAZ20087	Aaz20087 pNOV3604	914	14.2	71.0	281	3	AAAC16894	Aaac16894 Human sec
C 842	14.4	72.0	6103	2	AAZ20087	Aaz20087 Plasmid p	915	14.2	71.0	281	3	AAAC16894	Aaac16894 Human sec
C 843	14.4	72.0	6111	3	AAAS4211	Aaas4211 Transform	916	14.2	71.0	300	2	AAZ12644	Aaz12644 Human gen
C 844	14.4	72.0	6351	6	ABL33446	AbL33446 Human imm	917	14.2	71.0	315	3	AAF10224	Aaf10224 Fusarium
C 845	14.4	72.0	6351	6	ABK31335	Abk31335 Signal tr	918	14.2	71.0	323	10	ADD31107	Add31107 Rat cDNA
C 846	14.4	72.0	6351	6	ABL70299	AbL70299 Chemicall	919	14.2	71.0	323	10	ADD90796	Add90796 Rat RVP-1
C 847	14.4	72.0	6351	6	AAKS61231	Aas61231 Human gen	920	14.2	71.0	324	2	AAK84920	Aak84920 Interleuk
C 848	14.4	72.0	7195	4	AAD19823	Adad19823 pNOV2804	921	14.2	71.0	348	2	AAV35474	Aav35474 Human cDN
C 849	14.4	72.0	7247	5	ADM20200	Adm20200 Alternati	922	14.2	71.0	354	2	AAV34950	Aav34950 Human cDN
C 850	14.4	72.0	8144	2	AAK32482	Aak32482 Porcine a	923	14.2	71.0	363	9	ACH30717	Ach30717 Human bon
C 851	14.4	72.0	9172	4	AAD19836	Aad19836 pNOV2117	924	14.2	71.0	366	2	AAT94062	Aat94062 Recombina
C 852	14.4	72.0	9546	12	ADNA0876	Adna0876 Plasmid p	925	14.2	71.0	368	8	ABX36858	Abx36858 Bovine ES
C 853	14.4	72.0	9555	12	ADNA0876	Adna0876 Plasmid p	926	14.2	71.0	369	2	AAT94062	Aat94062 Recombina
C 854	14.4	72.0	10604	12	ADNA0877	Adna0877 Plasmid p	927	14.2	71.0	369	11	ACH95605	Ach95605 Klebsiell
C 855	14.4	72.0	11127	6	AAD36967	Aad36967 Arabidops	928	14.2	71.0	380	10	ADD32304	Add32304 Human mit
C 856	14.4	72.0	1187	6	ABK28451	Abk28451 DNA trans	929	14.2	71.0	389	3	AAC22117	Aac22117 Human sec
C 857	14.4	72.0	11461	4	AAD02175	Aad02175 Plasmid p	930	14.2	71.0	393	2	AAT33894	Aat33894 Immunode
C 858	14.4	72.0	12766	4	AAD02174	Aad02174 Plasmid p	931	14.2	71.0	393	3	AAA35225	Aaa35225 Human ade
C 859	14.4	72.0	12817	6	ABK15668	Abk15668 Expressio	932	14.2	71.0	393	3	AAFP21347	Aafp21347 Human low
C 860	14.4	72.0	12949	3	AAAS4213	Aaas4213 Transform	933	14.2	71.0	393	10	ABZ97041	Abz97041 Human nuc
C 861	14.4	72.0	13182	10	ABX15028	Abx15028 Human gen	934	14.2	71.0	393	11	ABD20890	Abd20890 Human pul
C 862	14.4	72.0	13269	6	AAD36961	Aad36961 Maize ubi	935	14.2	71.0	406	4	AAI85634	Aai85634 Human pol
C 863	14.4	72.0	13274	6	ABK15666	Abk15666 Binary ve	936	14.2	71.0	413	4	AAI19470	Aai19470 Human bre
C 864	14.4	72.0	13829	11	ADN08781	Adn08781 Maize opt	937	14.2	71.0	415	6	AAK62771	Aak62771 cDNA sequ
C 865	14.4	72.0	14603	6	AAD36966	Aad36966 Maize ubi	938	14.2	71.0	427	9	ACH49336	Ach49336 Human leu
C 866	14.4	72.0	14945	6	AAD36965	Aad36965 Maize ubi	939	14.2	71.0	428	8	ABX35099	Abx35099 Human mus
C 867	14.4	72.0	15503	6	AAD36964	Aad36964 Maize ubi	940	14.2	71.0	428	8	ABX58087	Abx58087 cDNA enco
C 868	14.4	72.0	15643	6	AAD36963	Aad36963 Maize ubi	941	14.2	71.0	428	12	ADJ27814	Adj27814 Human mus
C 869	14.4	72.0	16179	6	AAD36962	Aad36962 Maize ubi	942	14.2	71.0	433	4	AAI36534	Aai36534 Human mus
C 870	14.4	72.0	23695	6	ABQ65981	Abq66981 Human mtl	943	14.2	71.0	433	8	ABX59522	Abx59522 cDNA enco
C 871	14.4	72.0	28965	10	ADC66716	Adc66716 Human GPC	944	14.2	71.0	433	12	ADJ30272	Adj30272 Human mus
C 872	14.4	72.0	40308	4	AAK69184	Aak69184 Human imm	945	14.2	71.0	447	9	ACH49409	Ach49409 Human leu
C 873	14.4	72.0	52242	9	ADA02666	Ada02666 Human MDM	946	14.2	71.0	452	9	ACH41263	Ach41263 Human foe
C 874	14.4	72.0	52242	10	ADB72404	Adb72404 Human MDM	947	14.2	71.0	463	10	ADF80050	Adf80050 Leukaemia
C 875	14.4	72.0	52242	10	ADB72404	Adb72404 Human MDM	948	14.2	71.0	464	9	ACL20648	Acl20648 DNA clone
C 876	14.4	72.0	61890	4	ABL16586	AbL16586 Drosophil	949	14.2	71.0	473	6	ABQ59742	Abq59742 Human col
C 877	14.4	72.0	84707	6	ABQ67196	Abq67196 Continuation (7 of	950	14.2	71.0	488	9	ACH43392	Ach43392 Human foe
C 878	14.4	72.0	110000	4	AAK95240	Aak95240 Continuation (11 o	951	14.2	71.0	488	9	ACL20634	Acl20634 DNA clone
C 879	14.4	72.0	110000	6	ABT00011	Abt00011 Continuation (11 o	952	14.2	71.0	490	8	ABZ54276	Abz54276 Aspergill
C 880	14.4	72.0	110000	6	ABT00011	Abt00011 Continuation (11 o	953	14.2	71.0	496	9	ACL20639	Acl20639 DNA clone
C 881	14.4	72.0	110000	6	ABT05241	Abt05241 Continuation (27 o	954	14.2	71.0	499	9	ACL20636	Acl20636 DNA clone
C 882	14.4	72.0	110000	6	ABT01503	Abt01503 Continuation (11 o	955	14.2	71.0	500	9	ACL20629	Acl20629 DNA clone
C 883	14.4	72.0	110000	12	ADH77486	Adh77486 Continuation (11 o	956	14.2	71.0	500	9	ACL20637	Acl20637 DNA clone
C 884	14.4	72.0	247682	12	ADL08109	Adl08109 Human gen	957	14.2	71.0	500	10	ADC03542	Adc03542 Human Na/
C 885	14.4	72.0	249487	6	ABN85733	Abn85733 Mouse gen	958	14.2	71.0	505	5	ACL77025	Acl77025 DNA enco
C 886	14.4	72.0	349980	5	ABF86431	Abf86431 Pyrococcu	959	14.2	71.0	505	9	ACL20626	Acl20626 DNA clone
C 887	14.2	71.0	25	10	ADC05773	Adc05773 Human Na/	960	14.2	71.0	509	10	ADC76655	Adc76655 DNA homol
C 888	14.2	71.0	25	10	ADC05770	Adc05770 Human Na/	961	14.2	71.0	509	10	ADK55419	Adk55419 Plant DNA
C 889	14.2	71.0	25	10	ADC05774	Adc05774 Human Na/	962	14.2	71.0	510	9	ACL20638	Acl20638 DNA clone
C 890	14.2	71.0	25	10	ADC05775	Adc05775 Human Na/	963	14.2	71.0	511	6	ABQ22941	Abq22941 Oligonucle
C 891	14.2	71.0	25	10	ADC05769	Adc05769 Human Na/	964	14.2	71.0	511	6	ABQ22940	Abq22940 Oligonucle
C 892	14.2	71.0	25	10	ADC05771	Adc05771 Human Na/	965	14.2	71.0	520	9	ACL20633	Acl20633 DNA clone
C 893	14.2	71.0	25	10	ADC05772	Adc05772 Human Na/	966	14.2	71.0	527	4	AAH72842	Aah72842 Human cer
C 894	14.2	71.0	59	8	ABZ20874	Abz20874 Maize Opi	967	14.2	71.0	542	9	ACL20646	Acl20646 DNA clone
C 895	14.2	71.0	106	10	ADC03526	Adc03526 Human Na/	968	14.2	71.0	543	9	ACL20644	Acl20644 DNA clone
C 896	14.2	71.0	156	6	ABN17349	Abn17349 Human ORF	969	14.2	71.0	547	9	ACL20659	Acl20659 DNA clone
C 897	14.2	71.0	198	6	ABQ97093	Abq97093 Mouse ES	970	14.2	71.0	556	9	ACL20658	Acl20658 DNA clone

971 14.2 71.0 559 4 ABL19047 Drosophil
 c 972 14.2 71.0 559 9 ABL20628 DNA clone
 c 973 14.2 71.0 563 9 ABL20635 DNA clone
 c 974 14.2 71.0 567 6 ABK53382 Human eos
 c 975 14.2 71.0 568 5 ABV05667 Human pro
 c 976 14.2 71.0 569 9 ABL20630 DNA clone
 c 977 14.2 71.0 570 9 ABL20627 DNA clone
 c 978 14.2 71.0 573 12 ACH74720 Human gen
 c 979 14.2 71.0 577 9 ABL20645 DNA clone
 c 980 14.2 71.0 585 9 ABL20643 DNA clone
 c 981 14.2 71.0 591 9 ABL20649 DNA clone
 c 982 14.2 71.0 598 4 AAH07187 Human cdn
 c 983 14.2 71.0 599 4 AAH02931 Human she
 c 984 14.2 71.0 600 9 ABL20654 DNA clone
 c 985 14.2 71.0 609 9 ABL20657 DNA clone
 c 986 14.2 71.0 612 6 ABK78758 Bacillus
 c 987 14.2 71.0 612 9 ABL20655 DNA clone
 c 988 14.2 71.0 620 9 ABL20656 DNA clone
 c 989 14.2 71.0 624 9 ABL20632 DNA clone
 c 990 14.2 71.0 638 9 ABL20640 DNA clone
 c 991 14.2 71.0 639 9 ABL20625 DNA clone
 c 992 14.2 71.0 648 12 ADJ39058 Plant cdn
 c 993 14.2 71.0 651 9 ABL20653 DNA clone
 c 994 14.2 71.0 659 9 ABL20631 DNA clone
 c 995 14.2 71.0 660 10 ADC76060 DNA homol
 c 996 14.2 71.0 662 5 ABV36615 Human pro
 c 997 14.2 71.0 670 9 ABL20647 DNA clone
 c 998 14.2 71.0 729 8 ACA37439 Prokaryot
 c 999 14.2 71.0 732 10 ADC76652 DNA homol
 1000 14.2 71.0 732 10 ADK59272 Plant DNA

ALIGNMENTS

RESULT 1
 ID ABL20628 standard; DNA; 20 BP.
 AC ABL20628;
 DT 05-NOV-2002 (first entry)
 DE Primer useful for familial dysautonomia allele genotype analysis.

XX Familial dysautonomia; Riley-Day syndrome;
 KW hereditary sensory neuropathy III; human; carrier; diagnosis;
 KW IkappaB kinase-complex associated protein; primer; SSCP;
 KW single-strand conformational polymorphism; ss.
 OS Homo sapiens.
 XX EPI225232-A2.
 FN 24-JUL-2002.
 PD 17-JAN-2002; 2002EP-00001232.
 PF 17-JAN-2001; 2001US-0262284P.
 PR (RUBI/) RUBIN B Y.
 XX (ANDE/) ANDERSON S L.
 PA Rubin BY, Anderson SL;
 PI WPI; 2002-601228/65.
 DR Detecting a polymorphism in a gene encoding the ikappaB kinase-complex-
 PT associated protein is used to diagnose and identify carriers of familial
 PT dysautonomia.
 PS Claim 7; Page 9; 16pp; English.
 XX

CC The invention provides a method for detecting a polymorphism linked to a
 CC gene associated with familial dysautonomia (FD). This involves detecting
 CC a disruptive mutation in a gene encoding the IkappaB kinase-complex-
 CC associated protein (IKAP) on chromosomes 9q31. Sequence analysis of the
 CC IKAP-encoding gene showed, in chromosomes with the major FD haplotype, a
 CC T to C transition in position 6 of the donor splice site of intron 20.
 CC This mutation (2507+6T to C) results in the generation of an IKAP mRNA in
 CC which exon 20 is spliced out along with intron 20. Sequence analysis of
 CC the IKAP gene of individuals heterozygous for the FD chromosome with the
 CC most common minor haplotype (minor 2) showed a G to C transversion of
 CC nucleotide 2390 in exon 19 of the reported IKAP cDNA, resulting in an
 CC Arg96Pro amino acid substitution and disruption of a consensus Ser/Thr
 CC kinase phosphorylation site. The present sequence is a primer that can be
 CC used in a claimed method for detecting a disruptive mutation in the IKAP
 CC gene, using single-strand conformational polymorphism (SSCP) analysis.
 CC The primer was used in the genotype analysis of FD alleles. Use with the
 CC primer given in ABN84787 yielded a 238 bp fragment. In a family with
 CC probands homozygous for the major haplotype, all affected individuals
 CC were homoallelic for 2507+6C to C and all the parents were heterozygous.
 CC In families with probands heterozygous for the major and minor 2 FD
 CC haplotypes, 1 parent and the proband were heterozygous for R696P and the
 CC other parent and the proband were heterozygous for 2507+6T to C. Analysis
 CC of 31 probands homozygous for the major FD haplotype showed that 100% of
 CC the probands were homozygous for 2507+6T to C, 100% of the parents were
 CC heterozygous for this mutation, and 4 siblings of the probands had FD and
 CC were homozygous for the FD haplotype and the 2507+6T to C mutation. Study
 CC of a random group of 619 individuals of Ashkenazi Jewish descent revealed
 CC the presence of 25 carriers of 2507+6T to C and 2 individuals with R696P.
 CC The method is useful for FD diagnosis and for identifying carriers of the
 CC condition
 XX
 SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTAAATGGAGAGTGGCT 20
 Db 1 GCAGTAAATGGAGAGTGGCT 20

RESULT 2
 ABQ80567
 ID ABQ80567 standard; DNA; 66479 BP.
 AC ABQ80567;
 XX
 DT 08-NOV-2002 (first entry)
 DE Mutant human IKKAP gene #2.
 XX
 XX Human; IKKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier; screening;
 KW FD2; mutation; gene; chromosome 9q31; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(33714,G)
 FT /*tag= a
 XX
 PN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US000473.
 XX
 PR 06-JAN-2001; 2001US-0260080P.
 XX
 XX (GEHC) GEN HOSPITAL CORP.
 PA
 XX

PI Slangenaupt S, Guesella JF;
XX WPI; 2002-674806/72.
DR
XX
XX New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
XX
XX
PS Claim 1; Page; 109pp; English.
XX
XX The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. The mutation associated with the major haplotype
CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKBKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC gene contains 37 exons and maps to chromosome 9q31. Note: the present
CC sequence was not shown in the specification, but was derived from the
CC human wild-type IKBKAP sequence given in Fig 6
XX
SQ Sequence 66479 BP; 18271 A; 12399 C; 14128 G; 21681 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 66479;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||
DB 33581 GCAGTTAATGGAGAGTGGCT 33600

RESULT 3
ABQ80566
ID ABQ80566 standard; DNA; 66479 BP.
XX
AC ABQ80566;
XX
DT 08-NOV-2002 (first entry)
XX
DE Mutant human IKBKAP gene #1.
XX
KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW FD1; mutation; gene; chromosome 9q31; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH mutation replace(34201,T)
FT /*tag= a
FT mutation replace(34201,T)
XX
PN WO200259381-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-0260080P.
XX
PA (GEO) GEN HOSPITAL CORP.
XX

PI Slangenaupt S, Guesella JF;
XX WPI; 2002-674806/72.
DR
XX
XX New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
XX
XX
PS Claim 1; Page; 109pp; English.
XX
XX The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. The mutation associated with the major haplotype
CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)
CC in the IKBKAP protein, which is predicted to disrupt a potential
CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC gene contains 37 exons and maps to chromosome 9q31. Note: the present
CC sequence was not shown in the specification, but was derived from the
CC human wild-type IKBKAP sequence given in Fig 6
XX
SQ Sequence 66479 BP; 18271 A; 12399 C; 14129 G; 21680 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 66479;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||
DB 33581 GCAGTTAATGGAGAGTGGCT 33600

RESULT 4
ABQ80568
ID ABQ80568 standard; DNA; 66479 BP.
XX
AC ABQ80568;
XX
DT 08-NOV-2002 (first entry)
XX
DE Mutant human IKBKAP gene #3.
XX
KW Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
KW FD1; mutation; gene; chromosome 9q31; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH mutation replace(33714,G)
FT /*tag= a
FT mutation replace(34201,T)
XX
PN WO200259381-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-0260080P.
XX

PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Slangenaupt S, Gusella JF;
 XX
 DR WPI; 2002-674806/72.
 XX
 PT New IKKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
 PT prenatal diagnosis.
 XX
 PS Claim 1; Page; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
 CC 223900]. It was found that mutations in the IKKAP gene (see ABQ80565)
 CC are associated with FD. The mutation associated with the major haplotype
 CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
 CC nucleotide located at bp 6 of intron 20 in the IKKAP gene is replaced
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
 CC patients, although they continue to express varying levels of wild-type
 CC message in a tissue-specific manner. The mutation associated with the
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
 CC This bp mutation causes an arginine to proline missense mutation (R696P)
 CC in the IKKAP protein, which is predicted to disrupt a potential
 CC phosphorylation site. The IKKAP nucleic acid sequences are useful for
 CC identifying a subject with FD and for rapid carrier screening. The IKKAP
 CC gene contains 37 exons and maps to chromosome 9q31. Note: the present
 CC sequence was not shown in the specification, but was derived from the
 CC human wild-type IKKAP sequence given in Fig 6
 XX
 SQ Sequence 66479 BP; 18271 A; 12400 C; 14128 G; 21680 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 66479;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 33581 GCAGTTAATGGAGAGTGGCT 33600
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 DB 33581 GCAGTTAATGGAGAGTGGCT 33600
 RESULT 5
 ID ABQ80565 standard; DNA; 66479 BP.
 XX
 AC ABQ80565;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Human IKKAP wild-type gene.
 XX
 KW Human; IKKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
 KW gene; chromosome 9q31; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200259381-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 07-JAN-2002; 2002WO-US000473.
 XX
 PR 06-JAN-2001; 2001US-0260080P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Slangenaupt S, Gusella JF;
 XX
 DR WPI; 2002-674806/72.

XX
 PT New IKKAP genes with mutations, useful for identifying a subject with
 PT familial dysautonomia (FD), or for rapid carrier screening in the
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
 PT prenatal diagnosis.
 XX
 PS Claim 1; Fig 6; 109pp; English.
 XX
 CC The present invention relates to methods and compositions useful for
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
 CC 223900]. It was found that mutations in the IKKAP gene (the present
 CC sequence) are associated with FD. The mutation associated with the major
 CC haplotype of FD, FD1 mutation, is a base pair (bp) mutation, where the
 CC thymine nucleotide located at bp 6 of intron 20 in the IKKAP gene is
 CC replaced with a cytosine. This results in skipping of exon 20 in the mRNA
 CC from FD patients, although they continue to express varying levels of
 CC wild-type message in a tissue-specific manner. The mutation associated
 CC with the minor haplotype, FD2 mutation, is a bp mutation, where the
 CC guanine nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a
 CC cytosine. This bp mutation causes an arginine to proline missense
 CC mutation (R696P) in the IKKAP protein, which is predicted to disrupt a
 CC potential phosphorylation site. The IKKAP nucleic acid sequences are
 CC useful for identifying a subject with FD and for rapid carrier screening.
 CC The IKKAP gene contains 37 exons and maps to chromosome 9q31
 XX
 SQ Sequence 66479 BP; 18271 A; 12398 C; 14129 G; 21681 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 6; Length 66479;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 DB 33581 GCAGTTAATGGAGAGTGGCT 33600
 RESULT 6
 ID AAK69857 standard; DNA; 22791 BP.
 XX
 AC AAK69857;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24669.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001354.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214885P.
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PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225276P.
PR 14-AUG-2000; 2000US-0225277P.
PR 14-AUG-2000; 2000US-0225278P.
PR 14-AUG-2000; 2000US-0225279P.
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PR 22-AUG-2000; 2000US-0226681P.
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PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234233P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234967P.
PR 25-SEP-2000; 2000US-0234968P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236328P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
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PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249266P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 24669; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially


```
Db      873 GCAGTCAATGGAGATGGCT 892
RESULT 9
ADL31281
ID      ADL31281 standard; cDNA; 2637 BP.
XX
XX      AC      ADL31281;
XX      DT      20-MAY-2004 (first entry)
XX      DE      Full length human cDNA clone SeqID 3314.
XX      KW      human; medicine; signal transduction; glycoprotein; transcription;
XX      KW      oligo-capping method; ss; gene.
XX      OS      Homo sapiens.
XX      PN      EPI396543-A2.
XX      PD      10-MAR-2004.
XX      PF      07-JUL-2000; 2003EP-00025638.
XX      PR      08-JUL-1999; 99JP-00194486.
XX      PR      11-JAN-2000; 2000JP-00118774.
XX      PR      02-MAY-2000; 2000JP-00183965.
XX      PR      07-JUL-2000; 2000EP-00114089.
XX      PA      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX      PI      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX      PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX      DR      WPI; 2004-204755/20.
XX      DR      P-PSDB; ADL31282.
XX      PT      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX      PT      length human cDNAs.
XX      PS      Example 1; SEQ ID NO 3314; 1340pp; English.
XX      CC      This invention relates to a novel primers useful for synthesizing full
XX      CC      length cDNA molecules that encode human proteins. Specifically, it refers
XX      CC      to secretory or membrane proteins that are potential therapeutic agents/
XX      CC      target molecules in the field of medicine, and in particular genes
XX      CC      encoding proteins that are associated with signal transduction.
XX      CC      glycoproteins and transcription. The present invention describes a method
XX      CC      for efficiently cloning a full length human cDNA from both the 5' and 3'
XX      CC      ends using the oligo-capping method. This polynucleotide sequence is a
XX      CC      full length human cDNA clone of the invention.
XX      SQ      Sequence 2637 BP; 716 A; 626 C; 586 G; 709 T; 0 U; 0 Other;
Query Match      84.0%; Score 16.8; DB 12; Length 2637;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GCAGTCAATGGAGATGGCT 20
Db      873 GCAGTCAATGGAGATGGCT 892
RESULT 10
AAZ77516
ID      AAZ77516 standard; cDNA; 2878 BP.
XX
XX      AC      AAZ77516;
XX      DT      10-APR-2000 (first entry)
XX      DE      Human ovarian tumor cDNA library derived EST fragment 67.
XX
```

```
KW      Expressed sequence tag; EST; human; ovarian tumor; anticancer;
KW      gene therapy; treatment; ss.
XX      OS      Homo sapiens.
XX      PN      DE19817557-A1.
XX      PD      21-OCT-1999.
XX      PF      09-APR-1998; 98DE-01017557.
XX      PR      09-APR-1998; 98DE-01017557.
XX      PR      (META-) METAGEN GBS GENOMFORSCHUNG MBH.
XX      PA      Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX      PI      WPI; 1999-591920/51.
XX      DR      WPI; 1999-591920/51.
XX      PT      New nucleic acid sequences expressed in ovarian, and some other, cancer
XX      PT      tissues, and derived polypeptides, for treatment of ovarian cancer and
XX      PT      identification of therapeutic agents.
XX      PS      Claim 3; Page 193; 310pp; German.
XX      CC      This invention describes novel nucleic acid (cDNA) sequences (A) which
XX      CC      have anticancer activity and are highly expressed in ovarian tumor tissue
XX      CC      (and some also in testis and breast cancer tissue). The products of the
XX      CC      invention can be used for gene therapy. (A) are used (i) for recombinant
XX      CC      expression of polypeptides (B) and (ii) to isolate complete genes. (B)
XX      CC      are used (i) to identify agents suitable for treatment of ovarian cancer;
XX      CC      (ii) for treating this form of cancer (including expression from
XX      CC      gene therapy vectors) and (iii) for generation of specific antibodies.
XX      CC      (A) are identified by assembling ESTs (expressed sequence tags) from a
XX      CC      particular tissue type before comparison of expression patterns. This
XX      CC      allows a significantly longer fragment of the gene to be revealed, so
XX      CC      should reduce the number of failures associated with the fact that ESTs
XX      CC      from different libraries may represent different parts of the same
XX      CC      unknown gene, distorting the estimated frequency of occurrence in a
XX      CC      particular tissue. AAZ77450-Z77572 represent the human ovarian tumor cDNA
XX      CC      library derived EST fragments described in the method of the invention
XX      CC      and encode the protein fragments represented in AAY76505-Y76638
XX      SQ      Sequence 2878 BP; 776 A; 680 C; 628 G; 794 T; 0 U; 0 Other;
Query Match      84.0%; Score 16.8; DB 2; Length 2878;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GCAGTCAATGGAGATGGCT 20
Db      193 GCAGTCAATGGAGATGGCT 212
RESULT 11
AAS83893
ID      AAS83893 standard; cDNA; 4071 BP.
XX
XX      AC      AAS83893;
XX      DT      13-FEB-2002 (first entry)
XX      DE      DNA encoding novel human diagnostic protein #19697.
XX      KW      Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX      KW      food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX      OS      Homo sapiens.
XX      PN      WO200175067-A2.
XX      PD      11-OCT-2001.
XX
```

PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649157.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI: 2001-639362/73.
 DR P-PSDB; ABG19706.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 19697; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4071 BP; 1115 A; 935 C; 935 G; 1086 T; 0 U; 0 Other;
 Query Match 84.0%; Score 16.8; DB 5; Length 4071;
 Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2;
 OY 1 GCAGTTAATGAGAGTGCT 20
 DB 1780 GCAGTCAATGAGAGTGCT 1799
 RESULT 12
 ABL61892
 ID ABL61892 standard; DNA; 4977 BP.
 XX
 AC ABL61892;
 XX
 XX 15-MAY-2002 (first entry)
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:229.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytoskeletal; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX

PF 30-MAY-2001; 2001WO-US010838.
 XX
 PR 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 26-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX
 XX (AVAL-) AVALON PHARM.
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI: 2002-188264/24.
 XX
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 XX Claim 1; SEQ ID NO 229; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous

CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX
 SQ Sequence 4977 BP; 1394 A; 1147 C; 1042 G; 1394 T; 0 U; 0 Other;
 Query Match 84.0%; Score 16.8; DB 6; Length 4977;
 Best Local Similarity 90.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2;
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 Db 4806 GCTGTTAATGGAGAGTGGCT 4825
 RESULT 13
 ABK84229
 ID ABK84229 standard; cDNA; 4977 BP.
 XX
 AC ABK84229;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #800.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 SS WO200228999-A2.
 XX
 PN 11-APR-2002.
 XX
 PD 03-OCT-2001; 2001WO-US030821.
 XX
 PF 03-OCT-2000; 2000US-0237189P.
 XX
 PR (GENE-) GENE LOGIC INC.
 XX
 PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX
 PI WPI; 2002-435328/46.
 XX
 DR Detecting granulocyte activation by detecting differential expression of
 XX genes associated with granulocyte activation, which serves as diagnostic
 XX markers that is useful for monitoring disease states and drug toxicity.
 XX
 PS Claim 1; SEQ ID NO 800; 114pp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing the
 CC expression level to an expression level in an unactivated GC, where
 CC differential expression of Gs is indicative of GCA. Also included are
 CC modulating (M2) GA by contacting GC with an agent that alters the
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent
 CC capable of modulating GCA or an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease using the gene expression
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease, by detecting the level of
 CC expression in a sample of the tissue of gene(s) from Gs, where the level
 CC of expression of the gene is indicative of inflammation; (4) treating
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease, by contacting a tissue having inflammation with an

CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
 CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
 CC for screening an agent capable of modulating GCA preferably in an
 CC inflammation in a tissue; M4 is useful for detecting an inflammation
 CC (especially chronic) in a tissue, an allergic response in a subject,
 CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
 CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
 CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
 CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
 CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and M5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4977 BP; 1394 A; 1147 C; 1042 G; 1394 T; 0 U; 0 Other;
 Query Match 84.0%; Score 16.8; DB 6; Length 4977;
 Best Local Similarity 90.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2;
 QY 1 GCAGTTAATGGAGAGTGGCT 20
 Db 4806 GCTGTTAATGGAGAGTGGCT 4825
 RESULT 14
 ADL83261
 ID ADL83261 standard; cDNA; 4977 BP.
 XX
 AC ADL83261;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human PRO84725 cDNA, SEQ ID 463.
 XX
 KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; cancer;
 KW immune-mediated inflammatory disease; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 SS WO2004024097-A2.
 XX
 PN 25-MAR-2004.
 XX
 PD 15-SEP-2003; 2003WO-US029097.
 XX
 PF 16-SEP-2002; 2002US-0411392P.
 XX
 PR (GETH) GENENTECH INC.
 XX
 PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
 XX Wu TD;
 XX
 DR WPI; 2004-329399/30.
 XX P-PSDB; ADL83262.
 XX
 CC New PRO polypeptide, useful for diagnosing and treating a B cell related
 CC disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 CC mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
 XX
 PS Claim 2; Fig 463; 695pp; English.
 XX
 CC The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
 CC antigen unresponsiveness, selective IGA deficiency, selective IGM
 CC deficiency, selective deficiency of IGG subclasses, immunodeficiency with

CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
 CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.

XX
 SQ Sequence 4977 BP; 1394 A; 1147 C; 1042 G; 1394 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 12; Length 4977;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
 |||||
 DB 4806 GCTGTTAATGGAGAGTGGCT 4825

RESULT 15
 ADP28873
 ID ADF28873 standard; DNA; 5115 BP.
 AC ADF28873;
 DT 12-FEB-2004 (first entry)
 DE Pig nor-1 nuclear receptor nucleic acid AJ011767.
 XX
 XX Pig; nor-1; nuclear receptor; receptor; leukaemia; gene therapy;
 KW cytostatic; haematopoietic cell; ds.
 XX
 OS Sus scrofa.
 XX
 XX WO2003088812-A2.
 XX
 PD 30-OCT-2003.
 XX
 XX 15-APR-2003; 2003WO-US011804.
 XX
 XX 17-APR-2002; 2002US-0373238P.
 XX
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX (UNIW) UNIV WASHINGTON.
 XX
 XX Mulligan SE, Conneely OM, Milbrandt J;
 DR GENBANK; AJ011767.

PT Inhibiting proliferation of a hematopoietic cell, useful for treating or
 PT preventing leukemia, comprises modulating the level or activity of nor-1
 PT and/or nur77 nuclear receptor.
 XX
 XX Disclosure; SEQ ID NO 8; 101pp; English.

PS The present sequence is that of pig nor-1 nuclear receptor nucleic acid
 CC AJ011767. Nor-1 has been identified as a molecular target for therapeutic
 CC intervention in the treatment of myeloid leukaemia. The invention
 CC provides methods of inhibiting the proliferation of a haematopoietic stem
 CC cell or a haematopoietic myeloid cell by modulating the level of a nor-1
 CC and/or nur77 nuclear receptor. This involves increasing the level of the
 CC receptor polypeptide or polynucleotide, e.g. by administration of a
 CC vector comprising the polynucleotide. A claimed method of treating
 CC leukaemia comprises modulating a nor-1 and/or nur77 nuclear receptor in a
 CC haematopoietic stem cell or myeloid cell. Also claimed are methods of
 CC identifying an upregulator of expression of nor-1 and/or nur77, of
 CC identifying a compound for the treatment of leukaemia, and of screening
 CC for a compound for treatment of leukaemia, and a mouse model for

CC leukaemia comprising a mouse having defective nor-1 and nur77 nucleic
 CC acid sequences.

SQ Sequence 5115 BP; 1417 A; 1196 C; 1089 G; 1412 T; 0 U; 1 Other;

Query Match 84.0%; Score 16.8; DB 10; Length 5115;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
 |||||
 DB 4908 GCTGTTAATGGAGAGTGGCT 4927

RESULT 16
 AAC77462
 ID AAC77462 standard; cDNA; 5157 BP.
 XX
 AC AAC77462;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF3017 polynucleotide sequence SEQ ID NO:6033.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antitumetic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

XX 02-APR-1999; 99US-0127636P.

XX 05-APR-1999; 99US-0127728P.

XX 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

XX P-PSDB; AAB43253.

XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

XX Claim 5; Page 5215-5218; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The

CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX
 SQ Sequence 5157 BP; 1442 A; 1171 C; 1104 G; 1440 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 3; Length 5157;
 Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
 ||||| ||||| ||||| |||||
 DB 1551 GCAGTCAATGGAGATGGCT 1570

RESULT 17
 AAX35732
 ID AAX35732 standard; cDNA; 5178 BP.
 AC AAX35732;
 DT 09-JUL-1999 (first entry)
 XX cDNA encoding a protein identified by the signal sequence trap method.
 XX
 XX Signal sequence trap method; SST method; immunisation; inhibition;
 KW infection; allergy; cancer; regulation; tissue formation; tissue repair;
 KW activin activity; inhibin activity; chemokine activity;
 KW cytokine activity; blood coagulation regulation; agonist; antagonist;
 KW metabolic disorder; hormonal disorder; immune disorder;
 KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;
 KW ss.

XX Homo sapiens.
 XX WO9918126-A1.
 XX 15-APR-1999.
 XX 06-OCT-1998; 98WO-JP004514.
 XX 07-OCT-1997; 97JP-00274674.
 XX (ONCY) ONO PHARM CO LTD.
 XX Fukushima D, Shibayama S, Tada H;

PI WPI; 1999-277254/23.
 DR P-PSDB; AAY02377.
 XX Polypeptides identified by the signal sequence trap method from a human
 PT cDNA library.
 XX

PS Claim 5; Page 186-189; 281pp; Japanese.
 XX
 XX AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
 CC (AAY02358-84) which are identified from a human placental cDNA library by
 CC the signal sequence trap (SST) method. The polypeptides have a broad
 CC range of physiological activity, including immunisation against and
 CC inhibition of infections, allergies and cancer; regulation of tissue
 CC formation and repair; activin/inhibin activity; chemokine/cytokine
 CC activity; blood coagulation regulation; and receptor/ligand agonist or
 CC antagonist activity. The polypeptides can be used for prevention and
 CC treatment of disorders including infections by bacteria, yeasts and

CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;
 CC immune disorders (including severe combined immunodeficiency (SCID) and
 CC AIDS; thrombosis; cancer; and traumatic or surgical wounds
 XX
 SQ Sequence 5178 BP; 1470 A; 1204 C; 1128 G; 1376 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 5178;
 Best Local Similarity 90.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
 ||||| ||||| ||||| |||||
 DB 3291 GCAGTCAATGGAGATGGCT 3310

RESULT 18
 AAX35733
 ID AAX35733 standard; cDNA; 5457 BP.
 XX
 AC AAX35733;
 XX
 DT 09-JUL-1999 (first entry)
 XX cDNA encoding a protein identified by the signal sequence trap method.
 XX

XX Signal sequence trap method; SST method; immunisation; inhibition;
 KW infection; allergy; cancer; regulation; tissue formation; tissue repair;
 KW activin activity; inhibin activity; chemokine activity;
 KW cytokine activity; blood coagulation regulation; agonist; antagonist;
 KW metabolic disorder; hormonal disorder; immune disorder;
 KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;
 KW ss.

XX Homo sapiens.
 XX WO9918126-A1.
 XX 15-APR-1999.
 XX 06-OCT-1998; 98WO-JP004514.
 XX 07-OCT-1997; 97JP-00274674.
 XX (ONCY) ONO PHARM CO LTD.
 XX Fukushima D, Shibayama S, Tada H;

PI WPI; 1999-277254/23.
 DR P-PSDB; AAY02377.
 XX Polypeptides identified by the signal sequence trap method from a human
 PT cDNA library.
 XX
 PS Claim 4; Page 190-201; 281pp; Japanese.

XX AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
 CC (AAY02358-84) which are identified from a human placental cDNA library by
 CC the signal sequence trap (SST) method. The polypeptides have a broad
 CC range of physiological activity, including immunisation against and
 CC inhibition of infections, allergies and cancer; regulation of tissue
 CC formation and repair; activin/inhibin activity; chemokine/cytokine
 CC activity; blood coagulation regulation; and receptor/ligand agonist or
 CC antagonist activity. The polypeptides can be used for prevention and
 CC treatment of disorders including infections by bacteria, yeasts and
 CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;
 CC immune disorders (including severe combined immunodeficiency (SCID) and
 CC AIDS; thrombosis; cancer; and traumatic or surgical wounds
 XX
 SQ Sequence 5457 BP; 1548 A; 1263 C; 1183 G; 1463 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 5457;
 Best Local Similarity 90.0%; Pred. No. 2.1e-02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20
DB 3298 GCAGTCAATGGAGATGCT 3317

RESULT 19

ABX62937
ID ABX62937 standard; cDNA; 5642 BP.

XX AC
XX ABX62937;

XX 25-FEB-2003 (first entry)

XX Human activated T cell cDNA #53.

XX T cell; gene; ss; differential expression; T cell activation;
KW antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy;
KW allergy; cancer; graft versus host disease; infection;
KW autoimmune disorder.

XX OS Homo sapiens.

XX FN US2002137077-A1.

XX PD 26-SEP-2002.

XX PF 25-OCT-2001; 2001US-00002600.

XX PR 25-OCT-2000; 2000US-0243521P.

XX PA (HOPK/) HOPKINS C M.

XX PA (PETE/) PETERSON D P.

XX PA (COCK/) COCKS B G.

XX PA (HAWK/) HAWKINS P R.

XX PI Hopkins CM, Peterson DP, Cocks BG, Hawkins PR;

XX WPI; 2003-102381/09.

XX New combination comprising several cDNAs that are differentially
PT expressed in activated T cells, useful for diagnosing, treating, staging
PT or monitoring treatment for allergy, cancer, infectious and/or autoimmune
PT disorders.

XX PS Claim 1; Page; 180pp; English.

XX This invention relates to the sequences of several cDNAs that are
CC differentially expressed in activated T cells. The sequences of the
CC invention may have antiallergic, cytostatic, immunosuppressive and
CC antimicrobial activity and may be used in gene therapy. The invention
CC also comprises a method for screening samples for differentially
CC expressed genes and a method for detecting these cDNAs by hybridisation.
CC The methods and compositions of the present invention are useful for
CC diagnosing, treating, staging or monitoring treatment for allergy,
CC cancer, chronic graft versus host disease, infectious and/or autoimmune
CC disorders. The present sequence represents a cDNA of the invention that
CC is differentially expressed in activated T cells

SQ Sequence 5642 BP; 1472 A; 1399 C; 1212 G; 1465 T; 0 U; 94 Other;

Query Match 84.0%; Score 16.8; DB 8; Length 5642;
Best Local Similarity 90.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20

DB 5472 GCTGTTAATGGAGAGTGCT 5491

RESULT 20

AAS65659
ID AAS65659 standard; cDNA; 5768 BP.

XX AAS65659;
XX 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #1463.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG01472.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 1; SEQ ID NO 1463; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 5768 BP; 1592 A; 1319 C; 1284 G; 1572 T; 0 U; 1 Other;

Query Match 84.0%; Score 16.8; DB 5; Length 5768;
Best Local Similarity 90.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20

DB 2298 GCAGTCAATGGAGATGCT 2317

RESULT 21

ADE25701
ID ADE25701 standard; cDNA; 5828 BP.

XX ADE25701;


```

XX 13-FEB-2002 (first entry)
XX DE
XX DNA encoding novel human diagnostic protein #2018.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS
XX Homo sapiens.
XX PN WO200175067-A2.
XX PD
XX 11-OCT-2001.
XX PF
XX 30-MAR-2001; 2001WO-US008631.
XX PR
XX 31-MAR-2000; 2000US-00540217.
XX PR
XX 23-AUG-2000; 2000US-00649167.
XX PA
XX (HYSE-) HYSEQ INC.
XX PI
XX Drmanac RT, Liu C, Tang YT;
XX WIPI; 2001-639362/73.
XX DR
XX P-PSDB; ABG02027.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS
XX Claim 1; SEQ ID NO 2018; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX CC coding sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6291 BP; 1685 A; 1444 C; 1467 G; 1694 T; 0 U; 1 Other;
XX
XX Query Match 84.0%; Score 16.8; DB 5; Length 6291;
XX Best Local Similarity 90.0%; Pred. No. 2.1e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GCAGTTAATGGAGAGTGGCT 20
XX ||||| ||||| ||||| |||||
XX 501 GCAGTCAATGGAGATGGCT 520
XX
XX RESULT 24
XX ACC72047
XX ID ACC72047 standard; DNA; 8426 BP.
XX KW
XX AC ACC72047;
XX XX
XX 08-JUN-2003 (first entry)
XX
XX Key Location/Qualifiers
XX CDS 162..6587

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XX DE
XX BCU0586 gene #SEQ ID 71.
XX
XX Breast cancer; cytostatic; gene therapy; antisense therapy; regulated;
XX KW drug discovery; clinical medicine; forensic medicine; gene;
XX KW chromosome 16q13; ds.
XX OS
XX Homo sapiens.
XX PN WO2003029421-A2.
XX PD
XX 10-APR-2003.
XX PF
XX 02-OCT-2002; 2002WO-US031287.
XX PR
XX 03-OCT-2001; 2001US-0326526P.
XX PR
XX 14-MAY-2002; 2002US-00144194.
XX PA
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX PI
XX Sun Z, Li X, Fan W, Kovacs KF, Jay G;
XX WIPI; 2003-381623/36.
XX DR
XX P-PSDB; ABR58313.
XX
XX New isolated human differentially-regulated breast cancer polynucleotide
XX PT and polypeptide, useful for diagnosing, staging, prognosticating,
XX PT preventing and/or treating diseases and conditions relating to breast
XX PT cancer.
XX PS
XX Claim 2; SEQ ID NO 71; 127pp + Sequence Listing; English.
XX
XX The invention relates to isolated polynucleotides which are
XX differentially-regulated in breast cancer. The methods and compositions
XX of the present invention are useful for detecting, diagnosing, staging,
XX CC monitoring, prognosticating, preventing and/or treating diseases and
XX CC conditions relating to breast cancer, and may be used in gene therapy or
XX CC antisense therapy. They can also be used in research, drug discovery,
XX CC clinical medicine and forensic medicine. Sequences given in records
XX CC ACC72012-ACC72074 represent polynucleotides of the invention that are
XX CC differentially-regulated in breast cancer. NOTE: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 8426 BP; 2370 A; 1928 C; 1856 G; 2272 T; 0 U; 0 Other;
XX
XX Query Match 84.0%; Score 16.8; DB 8; Length 8426;
XX Best Local Similarity 90.0%; Pred. No. 2.2e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GCAGTTAATGGAGAGTGGCT 20
XX ||||| ||||| ||||| |||||
XX 5501 GCAGTCAATGGAGATGGCT 5520
XX
XX RESULT 25
XX ABQ79531
XX ID ABQ79531 standard; DNA; 8490 BP.
XX AC
XX ABQ79531;
XX
XX 25-NOV-2002 (first entry)
XX
XX Human PNL3734 nucleotide sequence.
XX
XX SET; PNL2118; TTP; CIN85; PNL3734; TIAR; FUBP1; antiinflammatory;
XX KW antiarteriosclerotic; cardiant; nootropic; gene therapy; gene; human; ds.
XX OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 162..6587

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29-SEP-2000; 2000US-0236327P.
 29-SEP-2000; 2000US-0236367P.
 29-SEP-2000; 2000US-0236368P.
 29-SEP-2000; 2000US-0236369P.
 29-SEP-2000; 2000US-0236370P.
 02-OCT-2000; 2000US-0236802P.
 02-OCT-2000; 2000US-0237037P.
 02-OCT-2000; 2000US-0237038P.
 02-OCT-2000; 2000US-0237039P.
 02-OCT-2000; 2000US-0237040P.
 13-OCT-2000; 2000US-0239935P.
 13-OCT-2000; 2000US-0239937P.
 20-OCT-2000; 2000US-0240960P.
 20-OCT-2000; 2000US-0241221P.
 20-OCT-2000; 2000US-0241785P.
 20-OCT-2000; 2000US-0241786P.
 20-OCT-2000; 2000US-0241787P.
 20-OCT-2000; 2000US-0241808P.
 20-OCT-2000; 2000US-0241809P.
 20-OCT-2000; 2000US-0241825P.
 01-NOV-2000; 2000US-0244617P.
 08-NOV-2000; 2000US-0246474P.
 08-NOV-2000; 2000US-0246475P.
 08-NOV-2000; 2000US-0246476P.
 08-NOV-2000; 2000US-0246477P.
 08-NOV-2000; 2000US-0246478P.
 08-NOV-2000; 2000US-0246523P.
 08-NOV-2000; 2000US-0246524P.
 08-NOV-2000; 2000US-0246525P.
 08-NOV-2000; 2000US-0246526P.
 08-NOV-2000; 2000US-0246527P.
 08-NOV-2000; 2000US-0246528P.
 08-NOV-2000; 2000US-0246532P.
 08-NOV-2000; 2000US-0246609P.
 08-NOV-2000; 2000US-0246610P.
 08-NOV-2000; 2000US-0246611P.
 08-NOV-2000; 2000US-0246613P.
 17-NOV-2000; 2000US-0249207P.
 17-NOV-2000; 2000US-0249208P.
 17-NOV-2000; 2000US-0249210P.
 17-NOV-2000; 2000US-0249211P.
 17-NOV-2000; 2000US-0249212P.
 17-NOV-2000; 2000US-0249213P.
 17-NOV-2000; 2000US-0249214P.
 17-NOV-2000; 2000US-0249215P.
 17-NOV-2000; 2000US-0249216P.
 17-NOV-2000; 2000US-0249217P.
 17-NOV-2000; 2000US-0249218P.
 17-NOV-2000; 2000US-0249244P.
 17-NOV-2000; 2000US-0249245P.
 17-NOV-2000; 2000US-0249264P.
 17-NOV-2000; 2000US-0249265P.
 17-NOV-2000; 2000US-0249297P.
 17-NOV-2000; 2000US-0249299P.
 01-DEC-2000; 2000US-0250160P.
 01-DEC-2000; 2000US-0250391P.
 05-DEC-2000; 2000US-0251030P.
 05-DEC-2000; 2000US-0251988P.
 06-DEC-2000; 2000US-0256719P.
 08-DEC-2000; 2000US-0251475P.
 08-DEC-2000; 2000US-0251856P.
 08-DEC-2000; 2000US-0251868P.
 08-DEC-2000; 2000US-0251869P.
 08-DEC-2000; 2000US-0251989P.
 11-DEC-2000; 2000US-0251990P.
 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 29-SEP-2000; 2001-465460/50.
 Novel polypeptides useful for diagnosing, treating, preventing and/or
 prognosing disorders related to the proteins, including cancers, immune
 disorders and neuronal disorders.
 Claim 1; SEQ ID NO 1313; 880pp; English.
 The invention relates to novel isolated polypeptides (I), and
 polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 diagnosing, preventing and treating diseases including immune system
 disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 transplant rejections and graft versus host disease, infectious diseases
 (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 other blood-related disorders (sickle cell anaemia), myeloproliferative
 disorders, primary haematopoietic disorders, hyperproliferative disorders
 (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
 Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
 (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
 glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
 respiratory disorders, dermatological disorders, in wound healing,
 epithelial cell proliferation, endocrine disorders (e.g. Addison's
 disease), reproductive system disorders, gastrointestinal disorders
 (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
 B-cell responsiveness to pathogens, activators of T-cells, to induce
 higher affinity antibodies, and as a means to induce tumour proliferation
 in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
 AAS27850 represent novel signal transduction pathway protein coding
 sequences and PCR primers of the invention
 SQ Sequence 29220 BP; 7863 A; 6353 C; 6337 G; 8667 T; 0 U; 0 Other;
 Query Match 84.0%; Score 16.8; DB 4; Length 29220;
 Best Local Similarity 90.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGAGAGTGGCT 20
 ||| ||||| ||||| |||||
 Db 9230 GCGGTAATGAGAGTGGCT 9249
 RESULT 27
 AAS27652/c
 ID AAS27652 standard; DNA; 29220 BP.
 XX
 AC AAS27652;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1312.
 XX
 KW Neutropenic; cytostatic; dermatological; immunosuppressive; tumour;
 antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 immune system disorder; rheumatoid arthritis; inflammatory condition;
 organ transplant rejection; infection; hepatitis C; blood disorder;
 sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
 neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
 cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 reproductive system; gastrointestinal; liver disorder; AIDS; ds;
 acquired immune deficiency syndrome.
 XX Homo sapiens.
 OS
 XX WO200154733-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US0001312.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR

PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226272P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227003P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229503P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249298P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
XX PT prognosing disorders related to the proteins, including cancers, immune
XX PT disorders and neuronal disorders.

Claim 1; SEQ ID NO 1312; 880pp; English.

XX The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (e.g.
 CC Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
 CC respiratory disorders, dermatological disorders, in wound healing,
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders, gastrointestinal disorder
 CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce
 CC higher affinity antibodies, and as a means to induce tumour proliferation
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
 CC AAS27850 represent novel signal transduction pathway protein coding
 CC sequences and PCR primers of the invention

XX Sequence 29220 BP; 8660 A; 6345 C; 6354 G; 7861 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 4; Length 29220;
 Best Local Similarity 90.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGCT 20
 Db 19991 GCGGTAATGGAGAGTGCT 19972

RESULT 28
 ADB94455/c
 ID ADB94455 standard; DNA; 29220 BP.

XX ADB94455;

XX 04-DEC-2003 (first entry)

XX Novel human protein DNA #64.

XX ds; gene; human; autoimmune disease; Parkinson's disease; silicosis;
 KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
 KW immunosuppressive agent; adjuvant; enhance immune response;
 KW higher affinity antibody induction;
 KW increased serum immunoglobulin concentration.

XX Homo sapiens.

XX US2002168711-A1.

XX 14-NOV-2002.

XX 17-JAN-2001; 2001US-00764868.

XX 31-JAN-2000; 2000US-0179065P.

XX 28-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214886P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0228668P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0235834P.
 PR 23-SEP-2000; 2000US-0236327P.
 PR 23-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-719985/68.

PT New isolated polypeptide useful for diagnosing and treating
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's
 PT disease.

PS Disclosure; SEQ ID NO 1312; 345pp; English.

XX The invention relates to an isolated polypeptide. The polypeptide is
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition in a subject, by determining the presence or
 CC amount of expression of the polypeptide in a biological sample and
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition based on the presence or amount of expression of the
 CC polypeptide. The polypeptide is also useful for identifying a binding
 CC partner to the polypeptide, which involves contacting the polypeptide
 CC with a binding partner and determining whether the binding partner
 CC effects an activity of the polypeptide. The polypeptide or the nucleic
 CC acid encoding the polypeptide is useful for preventing, treating, or
 CC ameliorating a medical condition, which involves administering the
 CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
 CC is useful for diagnosing a pathological condition or a susceptibility to
 CC a pathological condition in a subject, which involves determining the
 CC presence or absence of a mutation in the nucleic acid, and diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC based on the presence or absence of the mutation. The polypeptide, the
 CC nucleic acid and an antibody to the polypeptide are useful for treating
 CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
 CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,

```
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents DNA encoding a novel human protein. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format direct from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20020168711.
XX
SQ Sequence 29220 BP; 8660 A; 6345 C; 6354 G; 7861 T; 0 U; 0 Other;
Query Match 84.0%; Score 16.8; DB 10; Length 29220;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATGGAGAGTGGCT 20
Db 19991 GCGGGTAATGGAGAGTGGCT 19972
RESULT 29
ADB94456
ID ADB94456 standard; DNA; 29220 BP.
XX
AC ADB94456;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human protein DNA #65.
XX
KW ds; gene; human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.
XX
OS Homo sapiens.
XX
XX US2002168711-A1.
XX
XX 14-NOV-2002.
XX
XX 17-JAN-2001; 2001US-00764868.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
XX
XX 28-JUN-2000; 2000US-0214886P.
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XX 07-JUL-2000; 2000US-0216647P.
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XX 07-JUL-2000; 2000US-0216880P.
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XX 11-JUL-2000; 2000US-0217487P.
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XX 14-JUL-2000; 2000US-0218290P.
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XX 26-JUL-2000; 2000US-0220963P.
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XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0224518P.
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XX 14-AUG-2000; 2000US-0224519P.
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XX 14-AUG-2000; 2000US-0225267P.
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XX 14-AUG-2000; 2000US-0225268P.
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XX 14-AUG-2000; 2000US-0225270P.
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XX 14-AUG-2000; 2000US-0225447P.
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XX 14-AUG-2000; 2000US-0225757P.
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XX 14-AUG-2000; 2000US-0225758P.
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XX 22-AUG-2000; 2000US-0226868P.
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XX 30-AUG-2000; 2000US-0228924P.
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XX 01-SEP-2000; 2000US-0229287P.
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XX 01-SEP-2000; 2000US-0229343P.
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XX 01-SEP-2000; 2000US-0229344P.
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XX 01-SEP-2000; 2000US-0229345P.
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XX 05-SEP-2000; 2000US-0229509P.
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XX 05-SEP-2000; 2000US-0229513P.
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XX 08-SEP-2000; 2000US-0231413P.
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XX 21-SEP-2000; 2000US-0234223P.
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XX 21-SEP-2000; 2000US-0234274P.
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XX 25-SEP-2000; 2000US-0234997P.
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PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-719985/68.
XX
XX New isolated polypeptide useful for diagnosing and treating
XX immunosuppressive conditions such as autoimmune disease and Parkinson's
XX disease.
XX
XX Disclosure; SEQ ID NO 1313; 345pp; English.
XX
XX The invention relates to an isolated polypeptide. The polypeptide is
XX useful for diagnosing a pathological condition or a susceptibility to a
XX pathological condition in a subject, by determining the presence or
XX amount of expression of the polypeptide in a biological sample and
XX diagnosing a pathological condition or a susceptibility to a pathological
XX condition based on the presence or amount of expression of the
XX polypeptide. The polypeptide is also useful for identifying a binding
XX partner to the polypeptide, which involves contacting the polypeptide
XX with a binding partner and determining whether the binding partner
XX effects an activity of the polypeptide. The polypeptide or the nucleic
XX acid encoding the polypeptide is useful for preventing, treating, or
XX ameliorating a medical condition, which involves administering the
XX polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
XX is useful for diagnosing a pathological condition or a susceptibility to
XX a pathological condition in a subject, which involves determining the
XX presence or absence of a mutation in the nucleic acid, and diagnosing a
XX pathological condition or susceptibility to a pathological condition
XX based on the presence or absence of the mutation. The polypeptide, the
XX nucleic acid and an antibody to the polypeptide are useful for treating
XX autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
XX disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
XX the nucleic acid and the antibody are useful as immunosuppressive agents,
XX as adjuvants to enhance immune responses, and as agents to induce higher
XX affinity antibodies and increase serum immunoglobulin concentrations. The
XX present sequence represents DNA encoding a novel human protein. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format direct from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20020168711.
XX
XX Sequence 29220 BP; 7863 A; 6353 C; 6337 G; 8667 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 10; Length 29220;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATGGAGAGTGGCT 20
Db 9230 GCGGGTAATGGAGAGTGGCT 9249
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RESULT 30
AAX57351
XX AAX57351 standard; DNA; 68940 BP.
XX AC AAX57351;
XX DT 16-AUG-1999 (first entry)
XX DE Human chromosome 6q27 tumour suppressor gene.
XX KW Tumour suppressor gene; chromosome 6q27; cancer; therapy; human; D6S297;
XX KW breast cancer; ovarian cancer; lymphoid cancer; marker; D6S193; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT exon 414..549
XX FT /*tag= a
XX FT complement(719..724)
XX FT /*tag= b
XX FT 1126..1220
XX FT repeat_region /*tag= c
XX FT /*note= "MIR repeat family"
XX FT replace(1128..T)
XX FT /*tag= d
XX FT /*note= "putative polymorphism, C in 52b3, T in pDJ84g15"
XX FT variation replace(1309..C)
XX FT /*tag= e
XX FT /*note= "putative polymorphism, A in 52b3, C in pDJ84g15"
XX FT variation replace(1920..T)
XX FT /*tag= f
XX FT /*note= "putative polymorphism, C in 52b3, T in pDJ84g15"
XX FT exon complement(2310..2482)
XX FT /*tag= g
XX FT 2749..2843
XX FT exon /*tag= h
XX FT variation replace(2984..T)
XX FT /*tag= i
XX FT /*note= "putative polymorphism, C in 52b3, T in pDJ84g15"
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XX FT /*tag= j
XX FT /*note= "trapped exon"
XX FT exon 3654..3793
XX FT /*tag= k
XX FT complement(4483..4532)
XX FT promoter /*tag= l
XX FT complement(4615..4664)
XX FT promoter /*tag= m
XX FT 4854..4903
XX FT promoter /*tag= n
XX FT 4898..4927
XX FT promoter /*tag= o
XX FT exon 4912..5093
XX FT /*tag= p
XX FT complement(5398..5563)
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XX FT /*note= "match: D6S193 microsatellite"
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XX FT /*tag= r
XX FT 5767..5816
XX FT promoter /*tag= s
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XX FT complement(6395..6438)
XX FT exon /*tag= u
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XX FT /*tag= w
XX FT complement(7237..7434)
XX FT exon

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FT /*tag= y
FT complement(8414..8447)
FT /*tag= z
FT 8530..8695
FT /*tag= aa
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FT /*note= "trapped exon"
FT 9351..9678
FT /*tag= ac
FT /*note= "trapped exon"
FT complement(9467..9583)
FT /*tag= ad
FT 9627..9678
FT /*tag= ae
FT complement(9636..9685)
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FT /*tag= ag
FT complement(10669..10761)
FT /*tag= ah
FT complement(10706..10761)
FT /*tag= ai
FT 11067..11368
FT repeat_region /*tag= aj
FT /*note= "Alu repeat family"
FT exon 11264..11315
FT /*tag= ak
FT polyA_site complement(12270..12275)
FT /*tag= al
FT promoter complement(12641..12690)
FT /*tag= am
FT exon 13800..14074
FT /*tag= an
FT /*note= "trapped exon"
FT exon complement(14197..14400)
FT /*tag= ao
FT repeat_region complement(14496..14601)
FT /*tag= ap
FT /*note= "LI repeat family"
FT exon complement(14607..14860)
FT /*tag= aq
FT /*note= "trapped exon"
FT 14930..14979
FT promoter /*tag= ar
FT variation replace(15091..G)
FT /*tag= as
FT /*note= "putative polymorphism, A in 52b3 and pDJ84g15, G in 255h6"
FT polyA_site complement(15609..15614)
FT repeat_region 16174..16451
FT /*tag= at
FT 16174..16451
FT /*tag= au
FT /*note= "Alu repeat family"
FT exon 16509..16559
FT /*tag= av
FT exon 16867..17013
FT /*tag= ax
FT /*note= "trapped exon"
FT exon complement(16867..16939)
FT /*tag= aw
FT /*note= "trapped exon"
FT 17288..17352
FT /*tag= ay
FT exon complement(17427..17606)
FT /*tag= az
FT 17647..17696
FT promoter /*tag= ba
FT complement(18367..18416)
FT /*tag= bb
FT complement(19301..19334)
FT exon
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WP AAK96733_14 1400001 1503900

Query Match: 84.0%; Score 16.8; DB 4; Length 110000;
Best Local Similarity 90.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
DB 53558 GCAAGTAATGGAGAGTGGCT 53539

RESULT 34
AAK96733_08/c
Continuation (9 of 15) of AAK96733 from base 800001 (Human neuregulin-1 gene.)
WP Sequence split into 15 fragments LOCUS AAK96733 Accession AAK96733
WP Fragment Name Begin End
WP AAK96733_00 1 110000
WP AAK96733_01 100001 210000
WP AAK96733_02 200001 310000
WP AAK96733_03 300001 410000
WP AAK96733_04 400001 510000
WP AAK96733_05 500001 610000
WP AAK96733_06 600001 710000
WP AAK96733_07 700001 810000
WP AAK96733_08 800001 910000
WP AAK96733_09 900001 1010000
WP AAK96733_10 1000001 1110000
WP AAK96733_11 1100001 1210000
WP AAK96733_12 1200001 1310000
WP AAK96733_13 1300001 1410000
WP AAK96733_14 1400001 1503900

Query Match: 84.0%; Score 16.8; DB 4; Length 110000;
Best Local Similarity 90.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
DB 84752 GCAAGTAATGGAGAGTGGCT 84752

RESULT 35
ABT00010_04/c
Continuation (5 of 15) of ABT00010 from base 400001 (Human neuregulin-1 gene.)
WP Sequence split into 15 fragments LOCUS ABT00010 Accession ABT00010
WP Fragment Name Begin End
WP ABT00010_00 1 110000
WP ABT00010_01 100001 210000
WP ABT00010_02 200001 310000
WP ABT00010_03 300001 410000
WP ABT00010_04 400001 510000
WP ABT00010_05 500001 610000
WP ABT00010_06 600001 710000
WP ABT00010_07 700001 810000
WP ABT00010_08 800001 910000
WP ABT00010_09 900001 1010000
WP ABT00010_10 1000001 1110000
WP ABT00010_11 1100001 1210000
WP ABT00010_12 1200001 1310000
WP ABT00010_13 1300001 1410000
WP ABT00010_14 1400001 1503841

Query Match: 84.0%; Score 16.8; DB 6; Length 110000;
Best Local Similarity 90.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
DB 53558 GCAAGTAATGGAGAGTGGCT 53539

RESULT 36
ABT00010_08/c
Continuation (9 of 15) of ABT00010 from base 800001 (Human neuregulin-1 gene.)
WP Sequence split into 15 fragments LOCUS ABT00010 Accession ABT00010
WP Fragment Name Begin End
WP ABT00010_00 1 110000
WP ABT00010_01 100001 210000
WP ABT00010_02 200001 310000
WP ABT00010_03 300001 410000
WP ABT00010_04 400001 510000
WP ABT00010_05 500001 610000
WP ABT00010_06 600001 710000
WP ABT00010_07 700001 810000
WP ABT00010_08 800001 910000
WP ABT00010_09 900001 1010000
WP ABT00010_10 1000001 1110000
WP ABT00010_11 1100001 1210000
WP ABT00010_12 1200001 1310000
WP ABT00010_13 1300001 1410000
WP ABT00010_14 1400001 1503841

Query Match: 84.0%; Score 16.8; DB 6; Length 110000;
Best Local Similarity 90.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
DB 53558 GCAAGTAATGGAGAGTGGCT 53539

RESULT 37
ABT01503_04/c
Continuation (5 of 15) of ABT01503 from base 400001 (Human neuregulin-1 gene.)
WP Sequence split into 15 fragments LOCUS ABT01503 Accession ABT01503
WP Fragment Name Begin End
WP ABT01503_00 1 110000
WP ABT01503_01 100001 210000
WP ABT01503_02 200001 310000
WP ABT01503_03 300001 410000
WP ABT01503_04 400001 510000
WP ABT01503_05 500001 610000
WP ABT01503_06 600001 710000
WP ABT01503_07 700001 810000
WP ABT01503_08 800001 910000
WP ABT01503_09 900001 1010000
WP ABT01503_10 1000001 1110000
WP ABT01503_11 1100001 1210000
WP ABT01503_12 1200001 1310000
WP ABT01503_13 1300001 1410000
WP ABT01503_14 1400001 1503841

Query Match: 84.0%; Score 16.8; DB 6; Length 110000;
Best Local Similarity 90.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
DB 84772 GCAAGTAATGGAGAGTGGCT 84753

RESULT 38
ABT01503_08/c
Continuation (9 of 15) of ABT01503 from base 800001 (Human neuregulin-1 gene.)
WP Sequence split into 15 fragments LOCUS ABT01503 Accession ABT01503
WP Fragment Name Begin End
WP ABT01503_00 1 110000
WP ABT01503_01 100001 210000
WP ABT01503_02 200001 310000
WP ABT01503_03 300001 410000
WP ABT01503_04 400001 510000
WP ABT01503_05 500001 610000
WP ABT01503_06 600001 710000
WP ABT01503_07 700001 810000
WP ABT01503_08 800001 910000
```

Nucleotide sequence of the human musashi promoter.

XX Musashi promoter; multipotential neural progenitor cell;
 KW neural stem cell; central nervous system; ss.
 XX Homo sapiens.

OS WO200146384-A2.

PN 28-JUN-2001.

XX 22-DEC-2000; 2000WO-US035395.

PF 23-DEC-1999; 99US-0173003P.

PR (CORR) CORNELL RES FOUND INC.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA Goldman SA, Okano H;

XX WPI; 2001-418053/44.

XX Separating multipotential neural progenitor cells from a mixed population
 of cells, involves introducing nucleic acid molecule encoding fluorescent
 protein under promoter control, and separating fluorescent cells.

XX Claim 12; Fig 11A-JJ; 87pp; English.

XX The present sequence represents the human musashi promoter, which is used
 in the method of the invention. The specification describes a method for
 separating multipotential neural progenitor cells from a mixed population
 of cell types. The method comprises introducing a nucleic acid encoding a
 fluorescent protein under control of a promoter which selectively
 functions in the progenitor cells, into all cell types of the mixed
 population, allowing only the progenitor cells to express the fluorescent
 protein, and identifying and separating cells that are fluorescent, where
 the separated cells are progenitor cells. The method is useful for
 isolation and purification of multipotential neural progenitor cells,
 especially neural stem cells from adult brain. The isolated cells are
 used in both basic analyses of precursor and stem cell growth control, as
 well as in more applied studies of their transplantability and
 engraftment characteristics. The cells are useful in support of the
 structural repair of the damaged central nervous system, such as in the
 cord traumatized brain, or the contoured, traumatized or transected spinal
 cord

XX Sequence 52216 BP; 13494 A; 12461 C; 12362 G; 13699 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 4; Length 52216;

Best Local Similarity 94.4%; Pred. No. 4.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGG 18

Db 21276 GCAGTTAGTGGAGAGTGG 21293

RESULT 43

ABL50307

ID ABL50307 standard; DNA; 52216 BP.

XX ABL50307;

XX 13-JUN-2002 (first entry)

Human musashi promoter DNA sequence SEQ ID NO:1.

Human, musashi promoter; nestin enhancer; isolation; purification;

multipotential neural progenitor cell; neural progenitor cell; ds.

XX Homo sapiens.

XX JP2002034580-A.

PD 05-FEB-2002.

XX 05-JAN-2001; 2001JP-00000868.

XX 05-JAN-2000; 2000JP-00005307.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA (CORR) CORNELL RES FOUND INC.

XX WPI; 2002-275726/32.

XX Isolation and purification of multipotential neural progenitor cells and
 multipotential neural progenitor cells.

XX Claim 29; Page 14-31; 123pp; Japanese.

XX The present invention describes a method for separating multipotential
 neural progenitor cells from a mixed population of cell types in which a
 promoter functioning selectively in the neural progenitor cells is
 selected. A nucleic acid molecule encoding a fluorescent protein is
 introduced to all cell types of the mixed population of cell types under
 control of the promoter. Only the neural progenitor cells (not the other
 cell types) are allowed to express the fluorescent protein, cells of the
 mixed population of cell types that are fluorescent, which are restricted
 to the neural progenitor cells, are identified. The fluorescent cells are
 separated from the mixed population of cell types, the separated cells
 are restricted to the neural progenitor cells. The present invention also
 describes: (1) an isolated human musashi promoter; and (2) an enriched or
 purified preparation of isolated multipotential neural progenitor cells.
 The method is used for separating multipotential neural progenitor cells
 from a mixed population of cell types. The present sequence represents
 the human musashi promoter DNA sequence which can be used in the method
 of the invention

XX Sequence 52216 BP; 13494 A; 12460 C; 12362 G; 13900 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 52216;

Best Local Similarity 94.4%; Pred. No. 4.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGG 18

Db 21276 GCAGTTAGTGGAGAGTGG 21293

RESULT 44

AAI70577/c

ID AAI70577 standard; DNA; 29 BP.

XX AAI70577;

XX 21-JAN-2002 (first entry)

Human serine racemase PCR primer B.

Serine racemase; human; D-serine; regulation;
 glutamate N-methyl-D-aspartate receptor; neurodegenerative disease;
 stroke; Alzheimer's disease; Parkinson's disease; pain; myopathy;
 neotrophic; neuroprotective; cerebroprotective; antiparkinsonian;
 analgesic; diagnosis; gene therapy; screening; PCR primer; ss.

XX Homo sapiens.

XX WO200173077-A2.

XX 04-OCT-2001.

XX 30-MAR-2001; 2001WO-EP003668.

XX 31-MAR-2000; 2000US-0193748P.

XX 03-APR-2000; 2000US-0194249P.

XX (FARB) BAYER AG.

XX PI Ramakrishnan S;
XX DR WPI; 2001-648444/74.
XX PT Polynucleotide encoding serine racemase enzyme and the enzyme useful for
XX screening reagents regulating the activity of the enzyme in a neuron
XX PT disease caused by over- or under-activation of glutamate N-methyl-D-
XX aspartate.
XX PS Example 2; Page 51; 66pp; English.
XX CC The present sequence is that of primer B, designed for use with primer A
XX (see AA170575) in the PCR amplification of human serine racemase cDNA
XX (see AA170575). The expected size of the specific PCR product is 536 bp.
XX Human cDNA phage libraries were used as templates in PCR analysis in
XX order to determine the expression pattern of serine racemase mRNA in
XX human tissue. The invention provides methods of regulating serine
XX racemase activity in order to increase or decrease D-serine formation,
XX and thereby increase or decrease glutamate N-methyl-D-aspartate (NMDA)
XX receptor activation. A decrease in D-serine formation may aid in the
XX prevention of neuron damage following an ischaemic event, such as stroke.
XX Regulation of D-serine formation may also aid in the treatment of other
XX neurodegenerative conditions caused by the over- or under-activation of
XX the glutamate NMDA receptor
XX
XX SQ Sequence 29 BP; 10 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. NO. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TTAATGGAGAGTGGCT 20
DB 22 TTAATGGAGAGTGGCT 7
RESULT 45
AAAS9296
ID AAAS9296 standard; DNA; 509 BP.
XX AC AAAS9296;
XX XX 07-NOV-2000 (first entry)
XX DE C-terminal sequence of human serine racemase DNA.
XX XX Serine racemase; N-methyl-D-aspartate receptor; neural death;
XX KW neural dysfunction; NMDA receptor; Parkinson's disease;
XX KW Huntington's disease; motor neurone disease; Alzheimer's disease; ss.
XX OS Homo sapiens.
XX XX WO200043526-A1.
XX PN 27-JUL-2000.
XX PF 18-JAN-2000; 2000WO-US000938.
XX PR 19-JAN-1999; 99US-0116333P.
XX PR 21-JUL-1999; 99US-0144839P.
XX PR 28-JUL-1999; 99US-0145953P.
XX XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX XX Snyder SH, Wolosker H, Sheth K, Masaaki T, Mothet J, Brady RO;
XX PI Ferris CD;
XX XX WPI; 2000-482915/42.
XX XX Mammalian serine racemase preparations, used to identify modulators which
XX can be used to treat diseases associated with N-methyl-D-aspartate
XX PT receptor overactivation, e.g. Alzheimer's disease.

XX PS Claim 18; Page 27; 54pp; English.
XX CC The present sequence represents a fragment of a mammalian serine racemase
XX gene. The racemase polypeptide has a specific activity of at least 0.003
XX micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation
XX of L-serine to D-serine. D-serine appears to be an endogenous ligand of N
XX -methyl-D-aspartate (NMDA) receptors. The mammalian serine racemase can
XX be used to identify modulators, which can be used in the treatment of
XX acute or chronic neural death or dysfunction mediated by overactivation
XX of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors
XX is associated with Parkinson's disease, Huntington's disease, motor
XX neurone disease and Alzheimer's disease
XX
XX SQ Sequence 509 BP; 139 A; 90 C; 115 G; 164 T; 0 U; 1 Other;
Query Match 80.0%; Score 16; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. NO. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TTAATGGAGAGTGGCT 20
DB 441 TTAATGGAGAGTGGCT 456
RESULT 46
AA170575
ID AA170575 standard; cDNA; 1336 BP.
XX AC AA170575;
XX XX 21-JAN-2002 (first entry)
XX DE Human serine racemase cDNA.
XX XX Serine racemase; human; D-serine; regulation;
XX KW glutamate N-methyl-D-aspartate receptor; neurodegenerative disease;
XX KW stroke; Alzheimer's disease; Parkinson's disease; pain; myopathy;
XX KW neurotropic; neuroprotective; cerebroprotective; antiparkinsonian;
XX KW analgesic; diagnosis; gene therapy; screening; ss.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
XX FT CDS 52..1074
XX FT /*tag= a
XX
XX PN WO200173077-A2.
XX XX 04-OCT-2001.
XX PD 30-MAR-2001; 2001WO-EP003668.
XX PF 31-MAR-2000; 2000US-0193748P.
XX PR 03-APR-2000; 2000US-0194249P.
XX XX (FARB) BAYER AG.
XX XX Ramakrishnan S;
XX PI WPI; 2001-648444/74.
XX DR P-PSDB; AAAS0262.
XX XX Polynucleotide encoding serine racemase enzyme and the enzyme useful for
XX screening reagents regulating the activity of the enzyme in a neuron
XX PT disease caused by over- or under-activation of glutamate N-methyl-D-
XX aspartate.
XX PS Claim 1; Fig 1; 66pp; English.
XX CC The present sequence is that of cDNA encoding human serine racemase (see
XX AAAS0262). The polynucleotide can be used in the production of
XX recombinant serine racemase enzyme, or for the detection of serine

CC racemase polynucleotides. Expression vectors and host cells are claimed.
 CC Serine racemase catalyses the conversion of L-serine to D-serine. Neuron
 CC damage following various nervous system diseases is often caused by
 CC activation of glutamate N-methyl-D-aspartate (NMDA) receptors in the
 CC brain. This receptor is activated by the binding of D-serine. Regulation
 CC of D-serine levels through regulation of serine racemase may therefore
 CC prevent or minimize neuron damage in neurogenic and myopathic disorders,
 CC neurodegenerative disorders such as Alzheimer's disease and Parkinson's
 CC disease, and disorders leading to peripheral and chronic pain. Serine
 CC racemase polypeptides and polynucleotides are used in claimed methods of
 CC screening for agents that modulate or decrease the activity of serine
 CC racemase. Also claimed is a pharmaceutical composition comprising either
 CC an expression vector that contains a serine racemase polynucleotide, or a
 CC reagent that modulates serine racemase enzyme activity. This is used to
 CC modulate serine racemase activity in a disease, particularly neuron
 CC damage or a neurodegenerative disease caused by the over- or under-
 CC activation of the glutamate NMDA receptor

XX SQ Sequence 1336 BP; 386 A; 268 C; 319 G; 362 T; 0 U; 1 Other;

Query Match 80.0%; Score 16; DB 4; Length 1336;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

QY 5 TTAATGGAGAGTGGCT 20

Db 1166 TTAATGGAGAGTGGCT 1181

RESULT 47

AAD14461
 ID AAD14461 standard; cDNA; 1770 BP.

XX AC AAD14461;

XX DT 15-NOV-2001 (first entry)

XX DE Human pyridoxal-phosphate dependent enzyme 22406 cDNA.

XX KW Human; pyridoxal phosphate dependent enzyme; neurotropic; neuroprotective;
 KW anticonvulsant; cerebroprotective; cardiant; vasotropic; gene therapy;
 KW epilepsy; Alzheimer's disease; chromosome 17; serine racemase; stroke;
 KW behavioural change; neurodegenerative disorder; schizophrenia; atresia;
 KW rheumatic heart failure; circulatory disorder; hepatic injury; jaundice;
 KW lung disorder; nodular hyperplasia; stenosis; skeletal muscle disorder;
 KW tumour; rhabdomyosarcoma; dermal fibroblast disorder; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 69..1091

XX FT /*tag= a

XX FT /product= "Human pyridoxal phosphate dependent enzyme"

XX FT 69..1088

XX FT /*tag= b

XX FT /note= "This region is specifically claimed as SEQ ID NO:

XX FT 3 in claim 1"

XX EW WO200160987-A1.

XX XX 23-AUG-2001.

XX XX 20-FEB-2001; 2001WO-US005365.

XX XX 17-FEB-2000; 2000US-0183208P.

XX XX (MILL-) MILLENNIUM PHARM INC.

XX XX Meyers RA, Rudolph-Owen LA;

XX XX WPI; 2001-529909/58.

XX XX P-PSDB; AAE08342.

XX XX

PT Novel polypeptide of the human pyridoxal phosphate dependent family
 PT useful in screening and detection assays and for treatment, e.g. of
 PT epilepsy and Alzheimer's.

XX PS Claim 1; Fig 1; 121pp; English.

XX CC The present sequence is a cDNA encoding human pyridoxal phosphate
 CC dependent enzyme 22406 which is a serine racemase. Human 22406 gene is
 CC located on chromosome 17 between D17S849 and D17S796. The protein 22406
 CC is a modulator of D-serine. D serine has been shown to modify behavioural
 CC changes associated with learning, memory and convulsions. Human 22046 and
 CC compounds that modulate the expression or activity are used to treat or
 CC diagnose neurodegenerative disorders including Alzheimer's disease.
 CC schizophrenia as well as quell anxiety and epilepsy and prevent damage
 CC from stroke as well as cardiac (heart failure, rheumatic heart failure)
 CC and circulatory disorders, liver disorders (benign enlargement, nodular
 CC lung disorders, prostate disorders (atresia, stenosis), skeletal muscle
 CC hyperplasia), colon disorders (rhabdomyosarcoma) and dermal fibroblast disorders.
 CC Human 22406 cDNA is also useful in gene therapy

XX SQ Sequence 1770 BP; 499 A; 379 C; 410 G; 482 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 5; Length 1770;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATGGAGAGTGGCT 20

Db 1183 TTAATGGAGAGTGGCT 1198

RESULT 48

ADD22938

ID ADD22938 standard; cDNA; 1770 BP.

XX AC ADD22938;

XX DT 15-JAN-2004 (first entry)

XX DE cDNA encoding human pyridoxal-phosphate dependent enzyme, 22406.

XX KW Human; pyridoxal-phosphate dependent enzyme; 22406; acyltransferase;
 KW 32447; ATPase; 7716; aminotransferase; 25233; ring finger protein; 8035;
 KW 84242; aminopeptidase; 55304; metalloproteinase; 52999;
 KW ADP-ribosyltransferase; 21999; melanoma associated antigen; 52020;
 KW heart failure; ischaemic heart disease; myocardial infarction;
 KW hypertension; pericarditis; atherosclerosis; hepatic failure;
 KW viral hepatitis; cancer; intracerebral haemorrhage; brain abscess;
 KW Alzheimer's disease; Pick disease; Parkinson's disease;
 KW Huntington's disease; amyotrophic lateral sclerosis;
 KW inflammatory bowel disease; Crohn's disease;

XX KW benign prostatic hypertrophy; systemic lupus erythematosus; cardiac;
 KW hepatotropic; virucide; cytostatic; cerebroprotective; neurotropic;
 KW neuroprotective; anticonvulsant; antiinflammatory; immunosuppressive;
 KW gene; ss.

XX OS Homo sapiens.

XX XX US2003064439-A1.

XX XX 03-APR-2003.

XX XX 07-JUN-2002; 2002US-00164966.

XX XX 17-FEB-2000; 2000US-0183208P.

XX XX 26-JUN-2000; 2000US-0214138P.

XX XX 20-JUL-2000; 2000US-0219740P.

XX XX 20-JUL-2000; 2000US-0220465P.

XX XX 29-NOV-2000; 2000US-0253878P.

XX XX 30-NOV-2000; 2000US-0250073P.

XX XX 30-NOV-2000; 2000US-0250338P.

XX XX 30-NOV-2000; 2000US-0250348P.

```

PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesising polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
XX Claim 8; SEQ ID NO 15148; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention
XX
XX Sequence 2477 BP; 738 A; 535 C; 524 G; 680 T; 0 U; 0 Other;
XX
XX Query Match 80.0%; Score 16; DB 4; Length 2477;
XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 TTAATGGAGAGTGGCT 20
XX | | | | | | | | | |
XX 1183 TTAATGGAGAGTGGCT 1198
XX
XX RESULT 50
XX ADI82482
XX ID ADI82482 standard; DNA; 2477 BP.
XX AC ADI82482;
XX XX
XX XX 22-APR-2004 (first entry)
XX
XX XX Human modifier of p21 (MP21) gene sequence SeqID48.
XX
XX p21 pathway modulating agent; assay system; MP21; cytostatic;
XX KW MP21 protein activity modulator; cancer; genetically modified animal;
XX XX human; gene; ds.
XX
XX OS Homo sapiens.
XX
XX XX WO2004005486-A2.
XX
XX XX 15-JAN-2004.
XX
XX XX 09-JUL-2003; 2003WO-US021510.
XX
XX

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PR 10-JUL-2002; 2002US-0394795P.
PR 07-AUG-2002; 2002US-0401739P.
PR 16-SEP-2002; 2002US-0411010P.
PR 30-DEC-2002; 2002US-0437158P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Friedman L, Kidd T, Roche S, Joo DM, Lickteig K;
PI Amundsen CD, Hai B, Zhang H, Adamkewicz JI, Hammonds GR,
XX
XX WPI; 2004-091358/09.
DR P-PSDB; ADI82543.
XX
PT Identifying a candidate p21 pathway modulating agent, useful for treating
PT a disease such as cancer, comprises contacting an assay system comprising
PT a MP21 polypeptide or nucleic acid with a test agent.
XX
PS Example 2; SEQ ID NO 48; 392pp; English.
XX
CC This invention relates to a novel candidate p21 pathway modulating agent
CC by contacting an assay system comprising an MP21 (modifier of p21)
CC polypeptide or nucleic acid with a test agent, where in the absence of
CC the test agent the system provides a reference activity and detecting a
CC test agent-biased activity of the assay system. The invention may be
CC useful for the production of compounds with a cytostatic activity through
CC modulation of MP21 protein activity. The MP21 polypeptide or nucleic acid
CC can be used for identifying MP21 modulating agents useful as therapeutic
CC targets for diagnosing cancer or treating disorders associated with
CC defective or impaired p21 and/or MP21 function. MP21 modulating agents
CC are useful in diagnosis, therapy, for example treating cancer, and
CC pharmaceutical development. The genetically modified animals may be used
CC for in vivo assays to test for activity of a candidate p21 modulating
CC agent, or to further assess the role of MP21 in a p21 pathway process.
CC The present sequence is that of a human MP21 gene which is an orthologue
CC of a Drosophila p21 modifier and which was used in the exemplification of
CC the invention.
XX
SQ Sequence 2477 BP; 738 A; 535 C; 524 G; 680 T; 0 U; 0 Other;
Query Match 80.0%; Score 16; DB 12; Length 2477;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 TTAATGGAGAGTGGCT 20
Db 1183 TTAATGGAGAGTGGCT 1198

```

Search completed: December 3, 2004, 02:25:23
 Job time : 317.789 secs

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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 23:31:20 ; Search time 626.579 Seconds
(without alignments)
1509.457 Million cell updates/sec

US-10-050-189a-8

Title:

Perfect score: 20

Sequence: 1 gcagtttaattgagagtggtgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*

1: gb-pa.*

2: gb-hcg.*

3: gb-in.*

4: gb-on.*

5: gb-ov.*

6: gb-pat.*

7: gb-ph.*

8: gb-pl.*

9: gb-pr.*

10: gb-ro.*

11: gb-sts.*

12: gb-sv.*

13: gb-un.*

14: gb-vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX481361 Sequence
2	20	100.0	66479	6	AX676048 Sequence
3	20	100.0	78376	9	AL359692 Human DNA
4	18.4	92.0	137930	2	AC141193 Rattus no
5	18.4	92.0	217073	2	AC114144 Rattus no
6	18.4	92.0	219359	10	AB070355 Mus muscu
7	17.4	87.0	6032	10	AB070355 Rattus no
8	17.4	87.0	53722	2	AC100641 Mus muscu
9	17.4	87.0	118968	9	HS798F18 Human DNA
10	17.4	87.0	153412	2	AC118949 Rattus no
11	17.4	87.0	170847	2	AL357135 Homo sapi
12	17.4	87.0	172869	2	AC136550 Rattus no
13	17.4	87.0	217844	2	AC135710 Rattus no
14	17.4	87.0	220270	2	AC133519 Mus muscu
15	17.4	87.0	252428	2	AC129361 Rattus no
16	17.4	87.0	252630	2	AC097422 Rattus no
17	17.4	87.0	286008	2	AC123476 Rattus no
18	17	85.0	578	11	G86517 S209F6502FD
19	17	85.0	3449	8	AK119449 Oryza sat

C	20	17	85.0	53724	2	AC131074
C	21	17	85.0	177660	5	BX276188 Mus muscu
C	22	17	85.0	178061	2	AC108432 Mus muscu
C	23	17	85.0	184975	9	HS435D1 Human DNA
C	24	17	85.0	208657	2	AC046179 Homo sapi
C	25	17	85.0	226567	10	AC093316 Mus muscu
C	26	17	85.0	232203	2	AC127933 Rattus no
C	27	17	85.0	247342	2	AC103284 Rattus no
C	28	17	85.0	247649	2	AC111661 Rattus no
C	29	17	85.0	267852	2	AC126699 Rattus no
C	30	17	85.0	270720	2	AC128661 Rattus no
C	31	17	85.0	274998	2	AC102634 Mus muscu
C	32	17	85.0	282383	2	AC098451 Rattus no
C	33	17	85.0	346077	2	AC106235 Rattus no
C	34	16.8	84.0	2189	6	CQ834336 Sequence
C	35	16.8	84.0	2195	6	CQ834338 Sequence
C	36	16.8	84.0	2637	6	CQ783174 Sequence
C	37	16.8	84.0	2637	6	BD127513 Primer fo
C	38	16.8	84.0	2637	6	BD127513 Homo sapi
C	39	16.8	84.0	2878	6	BD203717 Human nuc
C	40	16.8	84.0	2878	6	AX014872 Sequence
C	41	16.8	84.0	3560	8	AF259793 Lycopersi
C	42	16.8	84.0	3572	9	AF259793 Homo sapi
C	43	16.8	84.0	4500	8	AF258808 Lycopersi
C	44	16.8	84.0	4517	8	AF258812 Lycopersi
C	45	16.8	84.0	4631	8	AF258809 Lycopersi
C	46	16.8	84.0	4977	6	AX329720 Sequence
C	47	16.8	84.0	4977	9	HSU12767 Human mitog
C	48	16.8	84.0	5115	4	SSC011767 Sus scrof
C	49	16.8	84.0	5122	6	CQ834342 Sequence
C	50	16.8	84.0	5137	9	BC024317 Homo sapi
C	51	16.8	84.0	5178	6	CQ755171 Sequence
C	52	16.8	84.0	5457	6	AX965632 Sequence
C	53	16.8	84.0	6518	9	AB023224 Homo sapi
C	54	16.8	84.0	7672	6	CQ834340 Sequence
C	55	16.8	84.0	7687	9	HSN804080 Homo sapi
C	56	16.8	84.0	7701	9	HSN804862 Homo sapi
C	57	16.8	84.0	7848	9	HSN805937 Homo sapi
C	58	16.8	84.0	9775	8	AF258813 Lycopersi
C	59	16.8	84.0	9775	2	AC069053 Homo sapi
C	60	16.8	84.0	60136	2	AC087480 Homo sapi
C	61	16.8	84.0	68940	9	AF019664 Homo sapi
C	62	16.8	84.0	75609	9	AC006456 Homo sapi
C	63	16.8	84.0	77332	9	AP006477 Homo sapi
C	64	16.8	84.0	77821	8	AC091627 Solanum d
C	65	16.8	84.0	83871	9	AC006599 Homo sapi
C	66	16.8	84.0	97037	9	AC004973 Homo sapi
C	67	16.8	84.0	101474	9	AF491780_04 Continuation (5 of
C	68	16.8	84.0	110000	9	AF491780_08 Continuation (9 of
C	69	16.8	84.0	110000	9	AF491780_08 Continuation (9 of
C	70	16.8	84.0	117149	9	AC083984 Homo sapi
C	71	16.8	84.0	135038	9	HUMYWD703 Homo sapi
C	72	16.8	84.0	146889	9	AL358937 Human DNA
C	73	16.8	84.0	149464	2	AC067800 Homo sapi
C	74	16.8	84.0	151938	9	HS323M4 Human DNA
C	75	16.8	84.0	155982	2	AC115929 Mus muscu
C	76	16.8	84.0	156938	9	AL159163 Human DNA
C	77	16.8	84.0	158759	2	AC136665 Rattus no
C	78	16.8	84.0	158811	9	AC004862 Homo sapi
C	79	16.8	84.0	159115	2	AC006406 Homo sapi
C	80	16.8	84.0	160766	2	AC137686 Homo sapi
C	81	16.8	84.0	162461	2	AC046166 Homo sapi
C	82	16.8	84.0	162974	2	AC046166 Homo sapi
C	83	16.8	84.0	163400	2	AC010364 Homo sapi
C	84	16.8	84.0	167478	2	AC067723 Homo sapi
C	85	16.8	84.0	167883	2	AC121026 Rattus no
C	86	16.8	84.0	169259	2	AC025806 Homo sapi
C	87	16.8	84.0	169511	9	AC146026 Pan trogl
C	88	16.8	84.0	171161	2	AC147084 Homo sapi
C	89	16.8	84.0	172464	2	AC140889 Homo sapi
C	90	16.8	84.0	177019	9	AC022833 Homo sapi
C	91	16.8	84.0	179465	2	AC027024 Homo sapi
C	92	16.8	84.0	180223	10	AL589692 Mouse DNA

c 93	16.8	84.0	181105	10	AC103367	AC103367 Mus muscu	166	16.4	82.0	211557	10	AC123605	AC123605 Mus muscu
c 94	16.8	84.0	181446	2	AC067813	AC067813 Homo sapi	c 167	16.4	82.0	213202	2	AC113484	AC113484 Homo sapi
c 95	16.8	84.0	181720	9	AC073283	AC073283 Homo sapi	c 168	16.4	82.0	218731	9	AC092033	AC092033 Homo sapi
c 96	16.8	84.0	182525	2	AC149761	AC149761 Bos tauru	c 169	16.4	82.0	220384	2	AC078926	AC078926 Homo sapi
c 97	16.8	84.0	184034	2	AC125163	AC125163 Mus muscu	c 170	16.4	82.0	220435	2	AC093468	AC093468 Mus muscu
c 98	16.8	84.0	187154	8	OSTN00107	AL065729 Oryza sat	c 171	16.4	82.0	221493	2	AC098143	AC098143 Rattus no
c 99	16.8	84.0	191317	2	AC150827	AC150827 Callithri	c 172	16.4	82.0	223337	10	AL928564	AL928564 Mouse DNA
c 100	16.8	84.0	194291	10	AC122330	AC122330 Mus muscu	c 173	16.4	82.0	225039	2	AC111941	AC111941 Rattus no
c 101	16.8	84.0	194429	2	AC146061	AC146061 Pan trogl	c 174	16.4	82.0	229488	2	AC097793	AC097793 Rattus no
c 102	16.8	84.0	195981	9	AC023948	AC023948 Homo sapi	c 175	16.4	82.0	235671	2	AC130022	AC130022 Rattus no
c 103	16.8	84.0	199239	2	AC093370	AC093370 Mus muscu	c 176	16.4	82.0	235993	2	AC118380	AC118380 Rattus no
c 104	16.8	84.0	204466	10	AC113463	AC113463 Mus muscu	c 177	16.4	82.0	237027	2	AC122580	AC122580 Rattus no
c 105	16.8	84.0	204651	10	AC090493	AC090493 Genomic s	c 178	16.4	82.0	237228	2	AC108615	AC108615 Rattus no
c 106	16.8	84.0	208651	10	AC087867	AC087867 Genomic s	c 179	16.4	82.0	237228	2	AC111654	AC111654 Rattus no
c 107	16.8	84.0	217281	10	AC087867	AC087867 Genomic s	c 180	16.4	82.0	247140	2	AC111654	AC111654 Rattus no
c 108	16.8	84.0	217392	2	AC107414	AC107414 Rattus no	c 181	16.4	82.0	247490	2	AC128155	AC128155 Rattus no
c 109	16.8	84.0	225940	10	AC116950	AC116950 Mus muscu	c 182	16.4	82.0	258939	2	AC110694	AC110694 Rattus no
c 110	16.8	84.0	225995	2	AC115153	AC115153 Rattus no	c 183	16.4	82.0	262239	2	AC147863	AC147863 Gallus ga
c 111	16.8	84.0	228287	2	AC103368	AC103368 Mus muscu	c 184	16.4	82.0	262239	2	AC114508	AC114508 Rattus no
c 112	16.8	84.0	229132	2	AC112047	AC112047 Rattus no	c 185	16.4	82.0	264661	2	AC103215	AC103215 Rattus no
c 113	16.8	84.0	229634	2	AC150010	AC150010 Callithri	c 186	16.4	82.0	264661	2	AC122319	AC122319 Mus muscu
c 114	16.8	84.0	236834	10	AC084073	AC084073 Mus muscu	c 187	16.4	82.0	265693	2	AC148331	AC148331 Mus muscu
c 115	16.8	84.0	238812	2	AC111727	AC111727 Rattus no	c 188	16.4	82.0	286346	2	AC101842	AC101842 Mus muscu
c 116	16.8	84.0	238922	2	AC097905	AC097905 Rattus no	c 189	16.4	82.0	301422	2	AC101842	AC101842 Mus muscu
c 117	16.8	84.0	238980	2	AC117863	AC117863 Rattus no	c 190	16.4	82.0	306788	1	AE016873	AE016873 Pseudonox
c 118	16.8	84.0	241875	2	AC123116	AC123116 Rattus no	c 191	16.4	82.0	310678	1	AE016873	AE016873 Pseudonox
c 119	16.8	84.0	248999	2	AC120992	AC120992 Rattus no	c 192	16.4	82.0	320658	2	AC145527	AC145527 Ateridox
c 120	16.8	84.0	262188	2	AC126973	AC126973 Rattus no	c 193	16.4	80.0	251	11	GL3303	GL3303 Human SIS W
c 121	16.8	84.0	273263	2	AC128458	AC128458 Rattus no	c 194	16.4	80.0	509	6	BD267509	BD267509 Mammalian
c 122	16.8	84.0	287427	2	AC108914	AC108914 Rattus no	c 195	16.4	80.0	1166	9	AF169974	AF169974 Homo sapi
c 123	16.8	84.0	301081	2	AC108658	AC108658 Rattus no	c 196	16.4	80.0	1336	6	AX259575	AX259575 Sequence
c 124	16.8	84.0	349980	6	AX282123	AX282123 Sequence	c 197	16.4	80.0	1770	6	AX234461	AX234461 Sequence
c 125	16.8	84.0	349980	6	AX282124	AX282124 Sequence	c 198	16.4	80.0	1770	6	AX224418	AX224418 Sequence
c 126	16.8	84.0	349980	6	AX282715	AX282715 Sequence	c 199	16.4	80.0	2264	9	HSM805450	HSM805450 Homo sapi
c 127	16.4	82.0	4025	10	AK173115	AK173115 Mus muscu	c 200	16.4	80.0	2477	6	BD158274	BD158274 Primer fo
c 128	16.4	82.0	4169	10	BC039919	BC039919 Mus muscu	c 201	16.4	80.0	2477	6	BD158274	BD158274 Primer fo
c 129	16.4	82.0	4176	10	BC039919	BC039919 Mus muscu	c 202	16.4	80.0	2973	5	BC073275	BC073275 Xenopus l
c 130	16.4	82.0	50916	2	AC100928	AC100928 Mus muscu	c 203	16.4	80.0	3798	9	BC019090	BC019090 Homo sapi
c 131	16.4	82.0	52216	6	BD012166	BD012166 Isolation	c 204	16.4	80.0	4107	9	AB037822	AB037822 Homo sapi
c 132	16.4	82.0	52216	6	BD128690	BD128690 Method fo	c 205	16.4	80.0	4140	9	AK026565	AK026565 Homo sapi
c 133	16.4	82.0	63107	9	AC079585	AC079585 Homo sapi	c 206	16.4	80.0	12460	6	AX344971	AX344971 Sequence
c 134	16.4	82.0	63107	9	AC079585	AC079585 Homo sapi	c 207	16.4	80.0	100725	2	AC149889	AC149889 Xenopus t
c 135	16.4	82.0	68291	2	AC103928	AC103928 Mus muscu	c 208	16.4	80.0	110000	8	CR380951	CR380951-5 Continuation (6 of
c 136	16.4	82.0	68291	2	AC103928	AC103928 Mus muscu	c 209	16.4	80.0	110000	8	CR380951	CR380951-5 Continuation (6 of
c 137	16.4	82.0	71909	2	AC100475	AC100475 Mus muscu	c 210	16.4	80.0	123454	2	AC149886	AC149886 Xenopus t
c 138	16.4	82.0	110000	2	AC110829	Continuation (5 of	c 211	16.4	80.0	123454	2	AC149886	AC149886 Xenopus t
c 139	16.4	82.0	121116	2	AC024661	Continuation (3 of	c 212	16.4	80.0	143468	9	AC113331	AC113331 Homo sapi
c 140	16.4	82.0	121116	2	AC024661	Continuation (3 of	c 213	16.4	80.0	147571	2	AC080177	AC080177 Homo sapi
c 141	16.4	82.0	13280	2	AC148282	AC148282 Homo sapi	c 214	16.4	80.0	149951	9	AC018375	AC018375 Homo sapi
c 142	16.4	82.0	143624	9	AC103288	AC103288 Homo sapi	c 215	16.4	80.0	159319	2	AL590419	AL590419 Homo sapi
c 143	16.4	82.0	143624	9	AC103288	AC103288 Homo sapi	c 216	16.4	80.0	161739	9	AC105277	AC105277 Homo sapi
c 144	16.4	82.0	150121	10	AC114925	AC114925 Homo sapi	c 217	16.4	80.0	162968	9	AC069303	AC069303 Homo sapi
c 145	16.4	82.0	152805	2	AC078923	AC078923 Homo sapi	c 218	16.4	80.0	162968	2	AC109794	AC109794 Bos tauru
c 146	16.4	82.0	153605	2	AC019360	AC019360 Homo sapi	c 219	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 147	16.4	82.0	153605	2	AC025255	AC025255 Homo sapi	c 220	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 148	16.4	82.0	153605	2	AC025255	AC025255 Homo sapi	c 221	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 149	16.4	82.0	163514	9	AC061869	AC061869 Homo sapi	c 222	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 150	16.4	82.0	163514	9	AC061869	AC061869 Homo sapi	c 223	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 151	16.4	82.0	184125	9	AC024257	AC024257 Homo sapi	c 224	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 152	16.4	82.0	187546	2	AC129236	AC129236 Homo sapi	c 225	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 153	16.4	82.0	187546	2	AC129236	AC129236 Homo sapi	c 226	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 154	16.4	82.0	187546	2	AC129236	AC129236 Homo sapi	c 227	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 155	16.4	82.0	187546	2	AC129236	AC129236 Homo sapi	c 228	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 156	16.4	82.0	190256	10	AC121302	AC121302 Mus muscu	c 229	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 157	16.4	82.0	193619	5	AL929464	AL929464 Zebrafish	c 230	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 158	16.4	82.0	201633	2	AC138639	AC138639 Mus muscu	c 231	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 159	16.4	82.0	203665	2	AC138677	AC138677 Mus muscu	c 232	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 160	16.4	82.0	204176	2	AC150393	AC150393 Branchios	c 233	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 161	16.4	82.0	204176	2	AC150393	AC150393 Branchios	c 234	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 162	16.4	82.0	204856	2	AC119275	AC119275 Mus muscu	c 235	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 163	16.4	82.0	208945	2	AC146022	AC146022 Pan trogl	c 236	16.4	80.0	166173	2	AC141418	AC141418 Pan trogl
c 164	16.4	82.0	209059	2	AC131670	AC131670 Mus muscu	c 237	15.8	79.0	171	6	C0751798	C0751798 Sequence
c 165	16.4	82.0	210126	2	AC128722	AC128722 Rattus no	c 238	15.8	79.0	197	11	G66222	G66222 s2373 YAC

C 239	15.8	79.0	318	6	AB3117471	AB3117471 Sequence	C 312	15.8	79.0	129398	9	AL596276	Human DNA
C 240	15.8	79.0	321	9	HS256VCI	Z3832 H. sapiens	313	15.8	79.0	129989	9	AC005681	Homo sapi
C 241	15.8	79.0	351	6	AB3117474	AB3117474 Sequence	C 314	15.8	79.0	130034	9	AC001726	Mus muscu
C 242	15.8	79.0	469	11	G36627	G36627 SHGC-53566	315	15.8	79.0	131611	9	AC005099	Homo sapi
C 243	15.8	79.0	631	11	G55510	G55510 SHGC-100858	316	15.8	79.0	132581	10	BX004977	Mouse DNA
C 244	15.8	79.0	780	6	AX868050	AX868050 Sequence	C 317	15.8	79.0	135660	2	AC103927	Mus muscu
C 245	15.8	79.0	780	6	BD148112	BD148112 Primer fo	C 318	15.8	79.0	135750	2	AC103927	Mus muscu
C 246	15.8	79.0	896	6	AX554778	AX554778 Sequence	C 319	15.8	79.0	137159	2	AL928859	Mouse DNA
C 247	15.8	79.0	998	6	AX554779	AX554779 Sequence	C 320	15.8	79.0	137828	8	AP006527	Oryza sat
C 248	15.8	79.0	1062	1	AY193149	AY193149 Unculture	C 321	15.8	79.0	138683	2	AC108193	Felis cat
C 249	15.8	79.0	1443	1	AY193152	AY193152 Unculture	C 322	15.8	79.0	139865	2	AC108899	Felis cat
C 250	15.8	79.0	1622	1	PRK2TRFA	X00713 Plasmid RK2	C 323	15.8	79.0	141121	10	AC099636	Mus muscu
C 251	15.8	79.0	1937	1	PRU05774	U05774 Plasmid RK2	C 324	15.8	79.0	141423	2	AC149570	Dasytus n
C 252	15.8	79.0	2051	8	RTAANTSNA	L34343 Ruta graveo	C 325	15.8	79.0	142116	9	AC034215	Homo sapi
C 253	15.8	79.0	2369	6	AE262494	AE262494 Sequence	C 326	15.8	79.0	143099	10	AC124431	Mus muscu
C 254	15.8	79.0	2369	6	AX023300	AX023300 Sequence	C 327	15.8	79.0	143432	2	AC115852	Mus muscu
C 255	15.8	79.0	2369	6	AX030767	AX030767 Sequence	C 328	15.8	79.0	144141	2	BX537151	Homo sapi
C 256	15.8	79.0	2369	6	BD007455	BD007455 Remedies	C 329	15.8	79.0	144734	2	AC148922	Dasytus n
C 257	15.8	79.0	2439	10	BC055100	BC055100 Mus muscu	C 330	15.8	79.0	146185	8	AP005651	Oryza sat
C 258	15.8	79.0	3319	9	AY679781	AY679781 Pan trogl	C 331	15.8	79.0	147490	9	AL445207	Human DNA
C 259	15.8	79.0	4321	6	CQ714104	CQ714104 Sequence	C 332	15.8	79.0	148565	2	AC022052	Homo sapi
C 260	15.8	79.0	4335	9	HSAF000996	AF000996 Homo sapi	C 333	15.8	79.0	149730	10	AL627229	Mouse DNA
C 261	15.8	79.0	4931	9	HSAF000995	AF000995 Homo sapi	C 334	15.8	79.0	150497	2	AC011860	Homo sapi
C 262	15.8	79.0	4939	10	BC059901	BC059901 Mus muscu	C 335	15.8	79.0	151079	9	AP001596	Homo sapi
C 263	15.8	79.0	5739	6	AX641842	AX641842 Sequence	C 336	15.8	79.0	155022	9	AC002395	Homo sapi
C 264	15.8	79.0	5739	10	AB023656	AB023656 Mus muscu	C 337	15.8	79.0	155038	2	AC124035	Rattus no
C 265	15.8	79.0	5743	9	AF131865	AF131865 Mus muscu	C 338	15.8	79.0	155249	2	AC126904	Rattus no
C 266	15.8	79.0	6476	9	HSAF000994	AF000994 Homo sapi	C 339	15.8	79.0	155287	5	AX119954	Zebrafish
C 267	15.8	79.0	9924	10	AF030130	AF030130 Mus muscu	C 340	15.8	79.0	156612	2	AC147212	Pan trogl
C 268	15.8	79.0	10098	1	AE015836	AE015836 Shewanell	C 341	15.8	79.0	158015	2	AC117771	Mus muscu
C 269	15.8	79.0	10390	1	AE013702	AE013702 Yersinia	C 342	15.8	79.0	159865	2	AC011568	Homo sapi
C 270	15.8	79.0	11237	12	AY204475	AY204475 Cloning v	C 343	15.8	79.0	160728	2	AC026816	Homo sapi
C 271	15.8	79.0	11503	1	AY135187	AY135187 Pseudomon	C 344	15.8	79.0	160872	10	AC131782	Mus muscu
C 272	15.8	79.0	15676	6	BD251968	BD251968 Artificia	C 345	15.8	79.0	161025	2	AC021276	Homo sapi
C 273	15.8	79.0	17111	6	BD251969	BD251969 Artificia	C 346	15.8	79.0	161686	10	AL627097	Mouse DNA
C 274	15.8	79.0	17116	6	BD251970	BD251970 Artificia	C 347	15.8	79.0	161735	9	AC068633	Homo sapi
C 275	15.8	79.0	19041	12	AF184978	AF184978 Cloning v	C 348	15.8	79.0	163849	2	AC044808	Mus muscu
C 276	15.8	79.0	27608	12	AF184978	AF184978 Binary ve	C 349	15.8	79.0	164014	10	AC138116	Mus muscu
C 277	15.8	79.0	28708	12	AY218787	AY218787 Cloning v	C 350	15.8	79.0	164028	9	AC004890	Homo sapi
C 278	15.8	79.0	35737	10	AL732315	AL732315 Mouse DNA	C 351	15.8	79.0	164046	2	AC135868	Rattus no
C 279	15.8	79.0	35913	2	AC149414	AC149414 Phakopsor	C 352	15.8	79.0	164102	2	AC149061	Mus muscu
C 280	15.8	79.0	36897	12	AB027255	AB027255 Cloning v	C 353	15.8	79.0	164608	2	AC147402	Dasytus n
C 281	15.8	79.0	39902	12	AB027254	AB027254 Cloning v	C 354	15.8	79.0	164795	9	AP002518	Homo sapi
C 282	15.8	79.0	40094	3	CEFA4F4	Z37092 Caenorhabdi	C 355	15.8	79.0	164909	2	AC101930	Mus muscu
C 283	15.8	79.0	40149	7	AY055382	AY055382 Salmonell	C 356	15.8	79.0	166782	2	AC132865	Mus muscu
C 284	15.8	79.0	43883	2	AC004396	AC004396 Pseudomon	C 357	15.8	79.0	167862	9	AC011966	Homo sapi
C 285	15.8	79.0	44645	9	AC108058	AC108058 Homo sapi	C 358	15.8	79.0	167957	2	AC011205	Homo sapi
C 286	15.8	79.0	51451	10	BX548165	BX548165 Mouse DNA	C 359	15.8	79.0	168259	2	AC009936	Homo sapi
C 287	15.8	79.0	55021	2	AC135004	AC135004 Rattus no	C 360	15.8	79.0	168278	10	AC16246	Mus muscu
C 288	15.8	79.0	60099	1	BIACOMGEN	I27758 Birmingham	C 361	15.8	79.0	168526	10	AC125185	Mus muscu
C 289	15.8	79.0	71179	2	AC100816	AC100816 Homo sapi	C 362	15.8	79.0	168986	2	AC110032	Mus muscu
C 290	15.8	79.0	74877	9	AL392088	AL392088 Human DNA	C 363	15.8	79.0	169586	9	AC078883	Homo sapi
C 291	15.8	79.0	76711	2	AC091341	Continuation (8 of	C 364	15.8	79.0	169701	2	AC128113	Rattus no
C 292	15.8	79.0	82140	10	BX539303	Continuation (8 of	C 365	15.8	79.0	170133	2	AC123327	Rattus no
C 293	15.8	79.0	82812	9	HSJ764022	HSJ764022 Mouse DNA	C 366	15.8	79.0	170342	10	AL929372	Mouse DNA
C 294	15.8	79.0	89039	5	AX548062	AX548062 Zebrafish	C 367	15.8	79.0	170385	2	BS000625	Pan trogl
C 295	15.8	79.0	90583	9	AC066024	AC066024 Homo sapi	C 368	15.8	79.0	170870	10	AC142270	Mus muscu
C 296	15.8	79.0	91048	9	AC008619	AC008619 Homo sapi	C 369	15.8	79.0	170960	2	AC026072	Homo sapi
C 297	15.8	79.0	108139	2	AC004085	Continuation (4 of	C 370	15.8	79.0	171006	10	AC109805	Mus muscu
C 298	15.8	79.0	108573	2	AC144760	AC144760 Medicago	C 371	15.8	79.0	172007	9	AC006376	Homo sapi
C 299	15.8	79.0	110000	1	AE017225	Continuation (51 o	C 372	15.8	79.0	172758	2	AC023553	Homo sapi
C 300	15.8	79.0	110000	1	AE017334	Continuation (51 o	C 373	15.8	79.0	173249	9	BS000208	Pan trogl
C 301	15.8	79.0	110000	1	AE017355	Continuation (51 o	C 374	15.8	79.0	173479	10	AC116798	Mus muscu
C 302	15.8	79.0	110000	2	LMF1CHR16_09	Continuation (4 of	C 375	15.8	79.0	174241	9	AC018634	Human Chr
C 303	15.8	79.0	110049	2	AC073746	Continuation (10 o	C 376	15.8	79.0	175291	2	AC024429	Homo sapi
C 304	15.8	79.0	115049	2	AC073746	Continuation (10 o	C 377	15.8	79.0	176282	2	AC068507	Homo sapi
C 305	15.8	79.0	118947	2	AC006321	AC006321 Homo sapi	C 378	15.8	79.0	176712	2	AC103290	Homo sapi
C 306	15.8	79.0	120612	9	BS000557	BS000557 Pan trogl	C 379	15.8	79.0	176755	8	AP005612	Oryza sat
C 307	15.8	79.0	12319	10	AL583830	AL583830 Mouse DNA	C 380	15.8	79.0	179233	9	AC095045	Homo sapi
C 308	15.8	79.0	123589	9	AC104790	AC104790 Homo sapi	C 381	15.8	79.0	179830	2	AC026344	Homo sapi
C 309	15.8	79.0	126086	2	AL731655	AL731655 Xenopus t	C 382	15.8	79.0	177830	2	AC123821	Mus muscu
C 310	15.8	79.0	126753	10	AL731655	AL731655 Mouse DNA	C 383	15.8	79.0	178671	10	AC124632	Mus muscu
C 311	15.8	79.0	127228	2	AC090057	AC090057 Oryza sat	C 384	15.8	79.0	178804	2	AC016918	Homo sapi

385	15.8	79.0	179429	2	AC120374	Mus muscu	AC120374	2	AC098139	Rattus no
386	15.8	79.0	179543	10	AC123822	Mus muscu	AC123822	5	AC132188	Pan trogl
387	15.8	79.0	179976	2	BX539318	Mus muscu	BX539318	5	EX005106	Zebrafish
388	15.8	79.0	180915	9	HS495919	Homo sapi	HS495919	2	AC106201	Rattus no
389	15.8	79.0	181226	9	AC012312	Homo sapi	AC012312	2	AC113299	Mus muscu
390	15.8	79.0	182114	2	AC026296	Homo sapi	AC026296	2	AC137132	Mus muscu
391	15.8	79.0	182423	10	AC126942	Mus muscu	AC126942	2	AC14584	Mus muscu
392	15.8	79.0	182525	2	AC149761	Bos tauru	AC149761	2	AC135652	Rattus no
393	15.8	79.0	182534	2	AC101948	Mus muscu	AC101948	2	AC098107	Rattus no
394	15.8	79.0	182758	2	AC138883	Homo sapi	AC138883	2	AC140483	Mus muscu
395	15.8	79.0	182769	9	AC146194	Homo sapi	AC146194	2	AC129871	Rattus no
396	15.8	79.0	183330	9	AC081372	Homo sapi	AC081372	2	AC115413	Rattus no
397	15.8	79.0	184000	9	AC087774	Homo sapi	AC087774	2	AC084210	Homo sapi
398	15.8	79.0	184105	2	AC144662	Rattus no	AC144662	2	AC094210	Homo sapi
399	15.8	79.0	186076	9	AC094101	Homo sapi	AC094101	2	AC103943	Rattus no
400	15.8	79.0	186777	2	AC094733	Rattus no	AC094733	2	AC115153	Rattus no
401	15.8	79.0	187714	2	AC148885	Otolemur	AC148885	2	AC096437	Rattus no
402	15.8	79.0	187977	10	AL672229	Mouse DNA	AL672229	2	AC097803	Rattus no
403	15.8	79.0	187988	9	AC009118	Homo sapi	AC009118	2	AC099077	Rattus no
404	15.8	79.0	189707	10	AC130551	Mus muscu	AC130551	2	AC134941	Rattus no
405	15.8	79.0	189841	5	AC147717	Gallus ga	AC147717	2	AC126289	Rattus no
406	15.8	79.0	190296	2	AC109276	Mus muscu	AC109276	2	AC096896	Rattus no
407	15.8	79.0	190846	9	AC006372	Homo sapi	AC006372	2	AC096896	Rattus no
408	15.8	79.0	190987	2	AC113883	Rattus no	AC113883	2	AC105632	Rattus no
409	15.8	79.0	192583	10	AL671782	Mouse DNA	AL671782	2	AC147994	Mus muscu
410	15.8	79.0	193005	10	AC131714	Mus muscu	AC131714	10	AC093043	Rattus no
411	15.8	79.0	193458	2	AC103676	Mus muscu	AC103676	2	AC126824	Rattus no
412	15.8	79.0	193787	2	AP000774	Homo sapi	AP000774	2	AL732546	Mouse DNA
413	15.8	79.0	193842	2	AC148903	Otolemur	AC148903	2	AC125268	Mus muscu
414	15.8	79.0	194994	2	AC134420	Mus muscu	AC134420	2	AC129419	Rattus no
415	15.8	79.0	195811	9	AC146098	Pan trogl	AC146098	2	AC129419	Rattus no
416	15.8	79.0	196102	10	AC124195	Mus muscu	AC124195	2	AC133664	Rattus no
417	15.8	79.0	196548	10	AL772242	Mouse DNA	AL772242	2	AC128048	Rattus no
418	15.8	79.0	197109	10	AL591542	Mus muscu	AL591542	2	AC120624	Rattus no
419	15.8	79.0	197190	10	AL591529	Homo sapi	AL591529	2	AC096493	Rattus no
420	15.8	79.0	198295	9	AC105129	Homo sapi	AC105129	2	AC139893	Rattus no
421	15.8	79.0	198375	10	AC120873	Mus muscu	AC120873	2	AC139893	Rattus no
422	15.8	79.0	198378	2	AC103657	Mus muscu	AC103657	2	AC117863	Rattus no
423	15.8	79.0	198637	9	HS315114	Mouse DNA	HS315114	2	AC094822	Rattus no
424	15.8	79.0	198693	10	AL672190	Mouse DNA	AL672190	2	AC126827	Rattus no
425	15.8	79.0	198949	9	AC010287	Homo sapi	AC010287	2	AC131583	Mus muscu
426	15.8	79.0	199287	2	AC068659	Homo sapi	AC068659	2	AC126848	Rattus no
427	15.8	79.0	199342	2	AC109105	Rattus no	AC109105	2	AC108559	Rattus no
428	15.8	79.0	201133	10	AL713915	Mouse DNA	AL713915	2	AC126529	Rattus no
429	15.8	79.0	201212	2	AC120380	Mus muscu	AC120380	2	AC16529	Rattus no
430	15.8	79.0	203027	2	AC120196	Gallus ga	AC120196	2	AC120235	Rattus no
431	15.8	79.0	202151	10	AC102358	Mus muscu	AC102358	2	AC150646	Bos tauru
432	15.8	79.0	202894	2	AC112611	Rattus no	AC112611	2	AC131536	Rattus no
433	15.8	79.0	203317	2	AC021062	Mus muscu	AC021062	2	AC106475	Rattus no
434	15.8	79.0	203763	2	AC123070	Mus muscu	AC123070	2	AC111872	Rattus no
435	15.8	79.0	203793	2	AC1016263	Homo sapi	AC1016263	2	CR382374	Danio rer
436	15.8	79.0	203849	2	AC119263	Mus muscu	AC119263	2	AC103170	Rattus no
437	15.8	79.0	205050	1	AJ414155	Yersinia	AJ414155	2	AC094659	Rattus no
438	15.8	79.0	206421	2	AC131110	Mus muscu	AC131110	2	AC098084	Rattus no
439	15.8	79.0	207633	2	AC103540	Mus muscu	AC103540	2	AC111634	Rattus no
440	15.8	79.0	207718	10	AL845262	Mouse DNA	AL845262	2	AC11282	Rattus no
441	15.8	79.0	208132	2	AC118860	Rattus no	AC118860	2	AC132548	Rattus no
442	15.8	79.0	208198	10	AC107664	Mus muscu	AC107664	2	AC021040	Homo sapi
443	15.8	79.0	209260	2	AC114156	Rattus no	AC114156	2	AC132638	Rattus no
444	15.8	79.0	209579	10	AC124764	Mus muscu	AC124764	2	AC132638	Rattus no
445	15.8	79.0	209820	10	AC138109	Mus muscu	AC138109	2	AL672086	Homo sapi
446	15.8	79.0	209875	10	AC132910	Mus muscu	AC132910	2	AC120697	Rattus no
447	15.8	79.0	209989	2	AC124427	Mus muscu	AC124427	2	AC170401	Bacillus
448	15.8	79.0	210427	10	AC124757	Mus muscu	AC124757	2	AC116207	Rattus no
449	15.8	79.0	210539	2	AC074161	Mus muscu	AC074161	2	AC138117	Mus muscu
450	15.8	79.0	210643	2	AC103432	Rattus no	AC103432	2	AC096514	Rattus no
451	15.8	79.0	210900	5	AL844193	Zebrafish	AL844193	2	AC102813	Mus muscu
452	15.8	79.0	212101	2	AC148782	Otolemur	AC148782	2	AC12813	Mus muscu
453	15.8	79.0	213049	2	AC079370	Mus muscu	AC079370	2	AC131145	Rattus no
454	15.8	79.0	213387	2	AC109275	Mus muscu	AC109275	2	AC129684	Rattus no
455	15.8	79.0	214795	2	AC132117	Mus muscu	AC132117	2	AC149054	Mus muscu
456	15.8	79.0	216342	9	AC109322	Homo sapi	AC109322	2	AC111798	Rattus no
457	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
458	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
459	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
460	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
461	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
462	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
463	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
464	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
465	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
466	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
467	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
468	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
469	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
470	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
471	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
472	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
473	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
474	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
475	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
476	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
477	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
478	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
479	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
480	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
481	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
482	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
483	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
484	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
485	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
486	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
487	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
488	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
489	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
490	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
491	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
492	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
493	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
494	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
495	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
496	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
497	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
498	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
499	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
500	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
501	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
502	15.8	79.0	215458	2	AC117798	Mus muscu	AC117798	2	AC11798	Rattus no
503	15.8	79.0	215458	2	AC					

C 531	15.8	79.0	305488	2	AC111881	AC111881 Rattus no	604	15.4	77.0	108893	9	HSDJ130E4	AL078582 Human DNA
C 532	15.8	79.0	308652	2	AC121478	AC121478 Rattus no	605	15.4	77.0	108895	9	AL137783	AL137783 Human DNA
C 533	15.8	79.0	321052	1	AB017281	AB017281 Bacillus	C 606	15.4	77.0	110000	2	AC108277	AC108277 Rattus no
C 534	15.8	79.0	340000	9	AF001696	AF001696 Homo sapi	C 607	15.4	77.0	110000	2	AC118787	Continuation (3 of
C 535	15.8	79.0	346553	2	AC102164	AC102164 Mus muscu	C 608	15.4	77.0	110000	2	AC121463	Continuation (3 of
C 536	15.4	77.0	56	6	BD274102	BD274102 Identific	C 609	15.4	77.0	110000	3	AE001572	AE001572 Drosophil
C 537	15.4	77.0	56	6	BD274119	BD274119 Identific	C 610	15.4	77.0	110000	8	AC145127	Continuation (14 o
C 538	15.4	77.0	306	6	CQ079965	CQ079965 Sequence	C 611	15.4	77.0	111350	9	AL157814	AL157814 Human DNA
C 539	15.4	77.0	306	6	CQ113738	CQ113738 Sequence	C 612	15.4	77.0	113146	9	AL354856	AL354856 Human DNA
C 540	15.4	77.0	306	6	CQ151610	CQ151610 Sequence	C 613	15.4	77.0	118404	4	AL773591	AL773591 Pig DNA s
C 541	15.4	77.0	306	6	CQ185327	CQ185327 Sequence	C 614	15.4	77.0	119666	9	HSDJ61B2	AL096710 Human DNA
C 542	15.4	77.0	306	6	CQ234987	CQ234987 Sequence	C 615	15.4	77.0	122228	9	AC000003	AC000003 Homo sapi
C 543	15.4	77.0	306	6	CQ272543	CQ272543 Sequence	C 616	15.4	77.0	123880	2	AC117928	AC117928 Gallus ga
C 544	15.4	77.0	306	6	CQ310196	CQ310196 Sequence	C 617	15.4	77.0	123880	2	AC117928	AC117928 Gallus ga
C 545	15.4	77.0	306	6	CQ346820	CQ346820 Sequence	C 618	15.4	77.0	125201	10	AL954334	AL954334 Mouse DNA
C 546	15.4	77.0	373	11	BV073001	BV073001 S212P6045	C 619	15.4	77.0	125201	3	AY319931	AY319931 Pristionc
C 547	15.4	77.0	464	6	CQ098119	CQ098119 Sequence	C 620	15.4	77.0	126255	3	AY319931	AY319931 Pristionc
C 548	15.4	77.0	464	6	CQ138066	CQ138066 Sequence	C 621	15.4	77.0	136158	2	AC141363	AC141363 Fells cat
C 549	15.4	77.0	464	6	CQ221451	CQ221451 Sequence	C 622	15.4	77.0	138020	3	AC024776	AC024776 Caenorhab
C 550	15.4	77.0	464	6	CQ297269	CQ297269 Sequence	C 623	15.4	77.0	142436	9	HSJ914N13	AL121575 Human DNA
C 551	15.4	77.0	464	6	CQ333602	CQ333602 Sequence	C 624	15.4	77.0	146576	8	AC074282	AC074282 Oryza sat
C 552	15.4	77.0	589	6	CQ070769	CQ070769 Sequence	C 625	15.4	77.0	146735	10	AL731728	AL731728 Mouse DNA
C 553	15.4	77.0	589	6	CQ098657	CQ098657 Sequence	C 626	15.4	77.0	149715	5	AL935049	AL935049 Zebrafish
C 554	15.4	77.0	589	6	CQ138642	CQ138642 Sequence	C 627	15.4	77.0	149787	9	AC016229	AC016229 Homo sapi
C 555	15.4	77.0	589	6	CQ175448	CQ175448 Sequence	C 628	15.4	77.0	150224	9	HSU1059L7	AL121913 Human DNA
C 556	15.4	77.0	589	6	CQ222057	CQ222057 Sequence	C 629	15.4	77.0	150794	9	AC025211	AC025211 Homo sapi
C 557	15.4	77.0	589	6	CQ260002	CQ260002 Sequence	C 630	15.4	77.0	152108	2	AC020282	AC020282 Drosophil
C 558	15.4	77.0	589	6	CQ297762	CQ297762 Sequence	C 631	15.4	77.0	152463	10	AC144808	AC144808 Mus muscu
C 559	15.4	77.0	589	6	CQ334126	CQ334126 Sequence	C 632	15.4	77.0	154123	2	AC019562	AC019562 Drosophil
C 560	15.4	77.0	672	11	BV048984	BV048984 S212P6025	C 633	15.4	77.0	154402	2	AC139634	AC139634 Gallus ga
C 561	15.4	77.0	1122	6	BD194623	BD194623 123 human	C 634	15.4	77.0	154809	10	AL645852	AL645852 Mouse DNA
C 562	15.4	77.0	1122	6	AL184094	AL184094 Sequence	C 635	15.4	77.0	159382	8	AC116601	AC116601 Oryza sat
C 563	15.4	77.0	2493	5	BC079785	BC079785 Xenopus 1	C 636	15.4	77.0	160853	9	AC093788	AC093788 Homo sapi
C 564	15.4	77.0	2706	9	AL161943	AL161943 Human DNA	C 637	15.4	77.0	161377	2	AC114625	AC114625 Mus muscu
C 565	15.4	77.0	2867	3	AB028055	AB028055 Giardia i	C 638	15.4	77.0	162380	2	AC148455	AC148455 Xenopus t
C 566	15.4	77.0	3501	3	AY095087	AY095087 Drosophil	C 639	15.4	77.0	163161	5	AL928928	AL928928 Zebrafish
C 567	15.4	77.0	5044	6	AB213219	AB213219 Sequence	C 640	15.4	77.0	163708	2	AC122791	AC122791 Mus muscu
C 568	15.4	77.0	5044	6	AB213219	AB213219 Sequence	C 641	15.4	77.0	163947	2	AC010964	AC010964 Homo sapi
C 569	15.4	77.0	5283	10	ACADL3	AF018435 Mus muscu	C 642	15.4	77.0	165212	10	AL956125	AL956125 Mouse DNA
C 570	15.4	77.0	6819	6	CQ069045	CQ069045 Sequence	C 643	15.4	77.0	165237	6	AX232505	AX232505 Sequence
C 571	15.4	77.0	7175	8	ALFACASE	L25042 Medicago sa	C 644	15.4	77.0	165549	9	AL355498	AL355498 Human DNA
C 572	15.4	77.0	9444	6	CQ069044	CQ069044 Sequence	C 645	15.4	77.0	165988	2	AC113573	AC113573 Canis fam
C 573	15.4	77.0	9974	1	AB013567	AB013567 Methanosa	C 646	15.4	77.0	166439	2	AL591722	AL591722 Homo sapi
C 574	15.4	77.0	13130	1	AB000040	AB000040 Mycoplasma	C 647	15.4	77.0	166559	2	CR450842	CR450842 Danio rer
C 575	15.4	77.0	23520	9	AC108028	AC108028 Homo sapi	C 648	15.4	77.0	167310	10	AC105169	AC105169 Mus muscu
C 576	15.4	77.0	31265	9	AL359880	AL359880 Human DNA	C 649	15.4	77.0	167384	10	AC138640	AC138640 Mus muscu
C 577	15.4	77.0	33834	2	AC017478	AC017478 Drosophil	C 650	15.4	77.0	168862	9	AC068058	AC068058 Homo sapi
C 578	15.4	77.0	37476	3	U40953	U40953 Caenorhabdi	C 651	15.4	77.0	169408	9	AC008573	AC008573 Homo sapi
C 579	15.4	77.0	41591	2	AC114429	AC114429 Homo sapi	C 652	15.4	77.0	169544	9	AC129967	AC129967 Sus scrofa
C 580	15.4	77.0	61505	9	AF305426	AF305426 Homo sapi	C 653	15.4	77.0	170784	2	AL161450	AL161450 Human DNA
C 581	15.4	77.0	63229	9	AC107938	AC107938 Homo sapi	C 654	15.4	77.0	171146	9	AL161450	AL161450 Human DNA
C 582	15.4	77.0	65116	2	AC100912	AC100912 Mus muscu	C 655	15.4	77.0	171188	10	AC134431	AC134431 Mus muscu
C 583	15.4	77.0	66800	10	AL732607	AL732607 Mouse DNA	C 656	15.4	77.0	171215	2	AX950173	AX950173 Danio rer
C 584	15.4	77.0	67004	2	AC102070	AC102070 Mus muscu	C 657	15.4	77.0	171520	2	AX950173	AX950173 Danio rer
C 585	15.4	77.0	67973	9	HSJ168B21	AL118518 Human DNA	C 658	15.4	77.0	173298	2	AC006489	AC006489 Drosophil
C 586	15.4	77.0	68778	2	AC130311	AC130311 Homo sapi	C 659	15.4	77.0	173538	9	AL158812	AL158812 Human DNA
C 587	15.4	77.0	72418	2	AC130311	AC130311 Homo sapi	C 660	15.4	77.0	173738	9	AL136132	AL136132 Human DNA
C 588	15.4	77.0	74673	9	AC005683	AC005683 Homo sapi	C 661	15.4	77.0	174080	2	AF217246	AF217246 Homo sapi
C 589	15.4	77.0	79150	3	AC002513	AC002513 Drosophil	C 662	15.4	77.0	174521	2	AC012466	AC012466 Homo sapi
C 590	15.4	77.0	80526	3	AC045976	AC045976 Gallus ga	C 663	15.4	77.0	174997	9	AC138089	AC138089 Homo sapi
C 591	15.4	77.0	80765	8	NCB1308	AL670008 Neurospor	C 664	15.4	77.0	175406	10	AC131778	AC131778 Mus muscu
C 592	15.4	77.0	82719	8	NCB1308	AL670008 Neurospor	C 665	15.4	77.0	176042	2	AC068966	AC068966 Homo sapi
C 593	15.4	77.0	86146	2	AC023805	AC023805 Mus muscu	C 666	15.4	77.0	176065	2	AC024046	AC024046 Homo sapi
C 594	15.4	77.0	87077	5	EX571732	EX571732 Zebrafish	C 667	15.4	77.0	176521	3	AC097725	AC097725 Drosophil
C 595	15.4	77.0	91436	8	NCB14A6	AL670007 Neurospor	C 668	15.4	77.0	177018	2	AC099716	AC099716 Mus muscu
C 596	15.4	77.0	92000	6	AR397408	Continuation (4 of	C 669	15.4	77.0	177060	2	AC150423	AC150423 Branchios
C 597	15.4	77.0	92019	9	AL450320	AL450320 Human DNA	C 670	15.4	77.0	177169	9	CNS01RGE	AL157955 Human chr
C 598	15.4	77.0	98133	10	AL627304	AL627304 Mouse DNA	C 671	15.4	77.0	177522	9	AC093566	AC093566 Homo sapi
C 599	15.4	77.0	99116	6	AF438683	AF438683 Sequence	C 672	15.4	77.0	178465	2	AP001901	AP001901 Homo sapi
C 600	15.4	77.0	99915	6	AX923386	AX923386 Sequence	C 673	15.4	77.0	179665	2	AC010246	AC010246 Homo sapi
C 601	15.4	77.0	101215	9	AC008966	AC008966 Homo sapi	C 674	15.4	77.0	179688	2	AC149625	AC149625 Papio anu
C 602	15.4	77.0	108136	10	AL606931	AL606931 Mouse DNA	C 675	15.4	77.0	180000	2	AC102737	AC102737 Mus muscu
C 603	15.4	77.0	108136	10	AL606931	AL606931 Mouse DNA	C 676	15.4	77.0	181570	2	AC068738	AC068738 Homo sapi

677	15.4	77.0	182712	9	AC018953	AC018953 Homo sapi	C 750	15.4	77.0	240507	2	AC103202	AC103202 Rattus no
c 678	15.4	77.0	183133	10	AC101851	AC101851 Mus muscu	C 751	15.4	77.0	244301	2	AC116072	AC116072 Rattus no
c 679	15.4	77.0	183735	9	AC011080	AC011080 Homo sapi	C 752	15.4	77.0	245369	2	AC125707	AC125707 Rattus no
c 680	15.4	77.0	184000	9	AC087774	AC087774 Homo sapi	C 753	15.4	77.0	246467	5	AL928716	AL928716 Zebrafish
c 681	15.4	77.0	184662	3	AC007692	AC007692 Drosophill	C 754	15.4	77.0	247830	2	AC118452	AC118452 Rattus no
c 682	15.4	77.0	185210	10	AL606910	AL606910 Mouse DNA	C 755	15.4	77.0	248479	10	AL807249	AL807249 Mouse DNA
c 683	15.4	77.0	185237	9	AC011124	AC011124 Homo sapi	C 756	15.4	77.0	253038	2	AC008930	AC008930 Homo sapi
c 684	15.4	77.0	186300	9	AL590730	AL590730 Human DNA	C 757	15.4	77.0	256998	10	AC115751	AC115751 Mus muscu
c 685	15.4	77.0	186744	9	AC116534	AC116534 Homo sapi	C 758	15.4	77.0	257686	2	AC115553	AC115553 Rattus no
c 686	15.4	77.0	187006	2	AC073602	AC073602 Mus muscu	C 759	15.4	77.0	258456	2	AC095604	AC095604 Rattus no
c 687	15.4	77.0	187364	2	AC120073	AC120073 Rattus no	C 760	15.4	77.0	259900	2	AC133278	AC133278 Rattus no
c 688	15.4	77.0	187508	2	AC021114	AC021114 Homo sapi	C 761	15.4	77.0	263434	2	AC135774	AC135774 Rattus no
c 689	15.4	77.0	188844	2	AC127475	AC127475 Canis fam	C 762	15.4	77.0	266022	2	AC095007	AC095007 Rattus no
c 690	15.4	77.0	189388	2	AC127475	AC127475 Canis fam	C 763	15.4	77.0	266342	2	AC109963	AC109963 Rattus no
c 691	15.4	77.0	190642	3	AC095307	AC095307 Mus muscu	C 764	15.4	77.0	271408	2	AC094667	AC094667 Rattus no
c 692	15.4	77.0	190867	9	AC095015	AC095015 Drosophill	C 765	15.4	77.0	274551	2	AC095227	AC095227 Rattus no
c 693	15.4	77.0	190994	10	AL845462	AL845462 Mouse DNA	C 766	15.4	77.0	279331	2	AC095172	AC095172 Rattus no
c 694	15.4	77.0	191207	2	AC021327	AC021327 Homo sapi	C 767	15.4	77.0	282416	2	AC124843	AC124843 Rattus no
c 695	15.4	77.0	192092	10	AC126248	AC126248 Mus muscu	C 768	15.4	77.0	282610	2	AC096244	AC096244 Rattus no
c 696	15.4	77.0	193047	9	CNS00000Q	AL049874 Human chr	C 769	15.4	77.0	297894	3	AE003477	AE003477 Drosophill
c 697	15.4	77.0	193377	2	AC135187	AC135187 Mus muscu	C 770	15.4	77.0	299140	2	AC110368	AC110368 Rattus no
c 698	15.4	77.0	194209	5	EX248318	EX248318 Zebrafish	C 771	15.4	77.0	299637	9	AY425004	AY425004 Homo sapi
c 699	15.4	77.0	194808	9	AC009987	AC009987 Homo sapi	C 772	15.4	77.0	300029	8	AE017051	AE017051 Oryza sat
c 700	15.4	77.0	197224	9	CNS01DUM	AL133279 Human chr	C 773	15.4	77.0	300958	2	AC096249	AC096249 Rattus no
c 701	15.4	77.0	197404	2	AC103636	AC103636 Mus muscu	C 774	15.4	77.0	308146	3	AE003673	AE003673 Drosophill
c 702	15.4	77.0	197810	9	AC090071	AC090071 Homo sapi	C 775	15.4	77.0	309026	2	AC006760	AC006760 Caenorhab
c 703	15.4	77.0	198318	2	AC095725	AC095725 Danio rer	C 776	15.4	77.0	309688	1	CR378571	CR378571 Photobact
c 704	15.4	77.0	200529	9	AC146447	AC146447 Pan trogl	C 777	15.4	77.0	349688	35	AR236137	AR236137 Sequence
c 705	15.4	77.0	201290	10	AL731682	AL731682 Mouse DNA	C 778	15.2	76.0	35	AR449016	AR449016 Sequence	
c 706	15.4	77.0	201602	2	AC074146	AC074146 Mus muscu	C 779	15.2	76.0	35	AR482418	AR482418 Sequence	
c 707	15.4	77.0	202317	9	AC020603	AC020603 Homo sapi	C 780	15.2	76.0	35	AR375332	AR375332 Sequence	
c 708	15.4	77.0	203179	2	AC109877	AC109877 Rattus no	C 781	15.2	76.0	35	BD006275	BD006275 Artificia	
c 709	15.4	77.0	203431	2	AC119313	AC119313 Rattus no	C 782	15.2	76.0	124	CQ709358	CQ709358 Sequence	
c 710	15.4	77.0	203849	2	AC118263	AC118263 Mus muscu	C 783	15.2	76.0	192	A75408	A75408 Sequence 10	
c 711	15.4	77.0	204167	2	AC114890	AC114890 Canis fam	C 784	15.2	76.0	192	A78387	A78387 Sequence 10	
c 712	15.4	77.0	204239	10	AC114819	AC114819 Mus muscu	C 785	15.2	76.0	249	AB115322	AB115322 Gallus ga	
c 713	15.4	77.0	204369	2	AC113314	AC113314 Mus muscu	C 786	15.2	76.0	300	CRS01APS	CRS01APS Botrytis	
c 714	15.4	77.0	204489	2	AL591117	AL591117 Homo sapi	C 787	15.2	76.0	308	AR236155	AR236155 Sequence	
c 715	15.4	77.0	204672	10	AC122831	AC122831 Mus muscu	C 788	15.2	76.0	308	AR449034	AR449034 Sequence	
c 716	15.4	77.0	207814	10	AL590994	AL590994 Mouse DNA	C 789	15.2	76.0	308	AR482436	AR482436 Sequence	
c 717	15.4	77.0	210232	9	AC010899	AC010899 Homo sapi	C 790	15.2	76.0	308	AX375422	AX375422 Sequence	
c 718	15.4	77.0	210863	10	AL772364	AL772364 Mouse DNA	C 791	15.2	76.0	308	BD006293	BD006293 Artificia	
c 719	15.4	77.0	212647	10	AL606987	AL606987 Mouse DNA	C 792	15.2	76.0	339	S60850	S60850 Ab2 heavy c	
c 720	15.4	77.0	213217	2	CR356230	CR356230 Danio rer	C 793	15.2	76.0	353	WU55552	WU55552 Mus muscu	
c 721	15.4	77.0	213831	2	AC094939	AC094939 Rattus no	C 794	15.2	76.0	357	BV121027	BV121027 PZA00926	
c 722	15.4	77.0	214037	2	AC021167	AC021167 Homo sapi	C 795	15.2	76.0	365	BV121025	BV121025 PZA00926	
c 723	15.4	77.0	214444	10	AC113287	AC113287 Mus muscu	C 796	15.2	76.0	368	BV121036	BV121036 PZA00926	
c 724	15.4	77.0	215716	10	AC140554	AC140554 Mus muscu	C 797	15.2	76.0	371	BV121028	BV121028 PZA00926	
c 725	15.4	77.0	216397	2	AC115199	AC115199 Rattus no	C 798	15.2	76.0	378	AX120585	AX120585 Unculture	
c 726	15.4	77.0	218922	2	AC008106	AC008106 Homo sapi	C 799	15.2	76.0	379	BV121038	BV121038 PZA00926	
c 727	15.4	77.0	220370	2	AC115382	AC115382 Rattus no	C 800	15.2	76.0	382	AX120589	AX120589 Unculture	
c 728	15.4	77.0	220612	2	AC119633	AC119633 Rattus no	C 801	15.2	76.0	382	AX120567	AX120567 Unculture	
c 729	15.4	77.0	222330	2	AC096255	AC096255 Rattus no	C 802	15.2	76.0	387	AX071797	AX071797 Sequence	
c 730	15.4	77.0	223146	2	AC134659	AC134659 Rattus no	C 803	15.2	76.0	445	AY454503	AY454503 Mus muscu	
c 731	15.4	77.0	225555	2	AC144789	AC144789 Gallus Ga	C 804	15.2	76.0	481	AY437075	AY437075 Mus muscu	
c 732	15.4	77.0	226076	3	AE003694	AE003694 Drosophill	C 805	15.2	76.0	492	BV121030	BV121030 PZA00926	
c 733	15.4	77.0	227054	9	AR172277	AR172277 Homo sapi	C 806	15.2	76.0	496	AF333777	AF333777 Pinus tae	
c 734	15.4	77.0	227138	2	AC094478	AC094478 Rattus no	C 807	15.2	76.0	498	BV121029	BV121029 PZA00926	
c 735	15.4	77.0	227924	2	AC148468	AC148468 Xenopus t	C 808	15.2	76.0	501	BV121032	BV121032 PZA00926	
c 736	15.4	77.0	228840	2	AC097835	AC097835 Rattus no	C 809	15.2	76.0	513	BV121031	BV121031 PZA00926	
c 737	15.4	77.0	229482	2	AC074149	AC074149 Mus muscu	C 810	15.2	76.0	513	BV121034	BV121034 PZA00926	
c 738	15.4	77.0	231919	2	AC111770	AC111770 Rattus no	C 811	15.2	76.0	514	BV121026	BV121026 PZA00926	
c 739	15.4	77.0	232817	2	AC102766	AC102766 Mus muscu	C 812	15.2	76.0	516	BV121035	BV121035 PZA00926	
c 740	15.4	77.0	234828	2	AC105862	AC105862 Rattus no	C 813	15.2	76.0	517	BV121033	BV121033 PZA00926	
c 741	15.4	77.0	234950	2	AC094003	AC094003 Rattus no	C 814	15.2	76.0	518	BV121037	BV121037 PZA00926	
c 742	15.4	77.0	235389	2	AC125746	AC125746 Rattus no	C 815	15.2	76.0	534	AY273198	AY273198 Enterobac	
c 743	15.4	77.0	235804	2	AC127084	AC127084 Rattus no	C 816	15.2	76.0	573	AX388972	AX388972 Sequence	
c 744	15.4	77.0	236809	2	AL356746	AL356746 Homo sapi	C 817	15.2	76.0	576	GG8655	GG8655 S210P625RB	
c 745	15.4	77.0	237313	5	AL845481	AL845481 Zebrafish	C 818	15.2	76.0	630	U89410	U89410 Mus muscu	
c 746	15.4	77.0	238255	2	AC132758	AC132758 Rattus no	C 819	15.2	76.0	670	BV045265	BV045265 S212P6043	
c 747	15.4	77.0	238632	2	CR392327	CR392327 Danio rer	C 820	15.2	76.0	756	Y18692	Y18692 Gallus gall	
c 748	15.4	77.0	240029	2	AC133810	AC133810 Rattus no	C 821	15.2	76.0	804	HSP2X4A3	HSP2X4A3 Human p2X4	
c 749	15.4	77.0	240200	2	AC116206	AC116206 Rattus no	C 822	15.2	76.0	839	BV026994	BV026994 S212P6968	

823	15.2	76.0	856	11	BV017711	BV017711 S212P6029	896	4217	10	BC046557	BC046557 Mus muscu
824	15.2	76.0	1002	6	E63790	E63790 Novel adeno	897	4269	3	LMLIPOPHO	AJ000010 Locusta m
C 825	15.2	76.0	1020	8	AY496050	AY496050 Phalaenop	C 898	4305	6	AX017140	AX017140 Sequence
826	15.2	76.0	1039	8	AY378148	AY378148 Phalaenop	C 899	4305	6	BD138480	BD138480 Fatty aci
827	15.2	76.0	1035	5	BX935664	BX935664 Gallus ga	900	4541	5	BC063744	BC063744 Danio rer
828	15.2	76.0	1047	14	AB182773	AB182773 Human ade	901	4543	10	AK173209	AK173209 Mus muscu
C 829	15.2	76.0	1128	6	C0715635	C0715635 Sequence	C 902	4560	9	HSN80330	HSN80330
C 830	15.2	76.0	1170	6	AR096541	AR096541 Sequence	903	4683	8	AF258810	AF258810 Lycopersi
C 831	15.2	76.0	1170	6	AR140077	AR140077 Sequence	904	4683	8	AF258810	AF258810 Lycopersi
C 832	15.2	76.0	1170	6	AR156655	AR156655 Sequence	905	4844	9	AL589667	AL589667 Human DNA
833	15.2	76.0	1255	8	AY122942	AY122942 Arabidops	C 906	4849	9	HSAC001556	HSAC001556 Homo sapi
834	15.2	76.0	1305	6	AB387774	AB387774 Sequence	C 907	5009	6	BD103191	BD103191 O-fucosyl
835	15.2	76.0	1332	6	AR387169	AR387169 Sequence	C 908	5189	9	D80002	D80002 Homo sapien
836	15.2	76.0	1431	6	C0598785	C0598785 Sequence	C 909	5249	9	AF375884	AF375884 Homo sapi
C 837	15.2	76.0	1456	6	AF199485	AF199485 Drosophill	C 910	5266	6	AX780153	AX780153 Sequence
838	15.2	76.0	1488	8	AY496051	AY496051 Phalaenop	C 911	5295	9	BC042491	BC042491 Homo sapi
839	15.2	76.0	1517	8	AY072119	AY072119 Arabidops	912	5295	9	BC042491	BC042491 Homo sapi
840	15.2	76.0	1522	14	AB023555	AB023555 Human ade	913	6591	8	AF258814	AF258814 Lycopersi
841	15.2	76.0	1522	14	AT317HG	AT317HG	C 914	7595	5	CHKNM5CB	M93676 Chicken non
842	15.2	76.0	1610	3	AY089481	AY089481 Drosophill	C 915	10645	1	AE003915	AE003915 Xylella f
843	15.2	76.0	1742	10	BC044489	BC044489 Mus muscu	C 916	11034	14	AF104985	AF104985 Hirame rh
844	15.2	76.0	1858	10	AF044058	AF044058 Rattus no	C 917	11163	1	AE004056	AE004056 Xylella f
C 845	15.2	76.0	1861	9	AF063598	AF063598 Homo sapi	918	11169	1	AE004388	AE004388 Vibrio ch
846	15.2	76.0	1903	10	BC078775	BC078775 Rattus no	C 919	11282	6	C0574856	C0574856 Sequence
847	15.2	76.0	2047	9	BC021138	BC021138 Homo sapi	C 920	12626	1	AE000803	AE000803 Methanoba
848	15.2	76.0	2092	10	BC034711	BC034711 Mus muscu	921	14006	6	AX346860	AX346860 Sequence
C 849	15.2	76.0	2097	3	AY095172	AY095172 Drosophill	C 922	14681	1	AE013893	AE013893 Yersinia
C 850	15.2	76.0	2097	8	CCL242497	A242497 Candida c	C 923	15668	2	AC012695	AC012695 Drosophill
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ALIGNMENTS

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 DEFINITION Sequence 8 from Patent EP1225232.
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 VERSION AX481361.1 GI:22315282
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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 Rubin, B.-K. and Anderson, S.L.
 Detection of mutations in a gene encoding lkbapp
 kinase-complex-associated protein to diagnose familial dysautonomia
 Patent: EP 1225232-A 8 24-JUL-2002;
 Rubin, Berish Y. (US); Anderson, Silvia L. (US)
 Location/Qualifiers
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 /mol_type="unassigned DNA"
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ORIGIN
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 Db 1 GCAGTTAATGGAGAGTGCGT 20

RESULT 2
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 LOCUS AX676048 DNA linear PAT 27-MAR-2003

DEFINITION Sequence 1 from Patent WO02059381.
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 VERSION AX676048.1 GI:29333739
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 Slagenhaupt, S. and Gusella, J.F.
 Gene for identifying individuals with familial dysautonomia
 TITLE Patent: WO 02059381-A 1 01-AUG-2002;
 JOURNAL The General Hospital Corporation (US)
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 DEFINITION sequence.
 ACCESSION AL359692
 VERSION AL359692.9 GI:14970800
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 78376)
 Sycamore, N.
 Direct Submission
 Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jul 19, 2001 this sequence version replaced gi:14715342.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr9
 RP11-3J11 is from the library PCPI-11.1 constructed by the group of
 Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm

VECTOR: PBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-3J11 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-3J11 is at 1 in this sequence. The true left end of clone RP11-115J22 is at 76377 in this sequence. The true right end of clone RP11-339N8 is at 76392 in this sequence.

FEATURES

Location/Qualifiers

source

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Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Sisson, I., Satter, C.D., Smajs, D., Sneed, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Soza, J., Steimle, M., Strong, R., Sutton, A.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D.,
Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,
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Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiser, R., Smith, D.R.,
Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 137930)
Worley, K.C.

Direct Submission
Submitted (10-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 137930)
Worley, K.C.

Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 11, 2003 this sequence version replaced gi:28894576.

----- Genome Center -----
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: KDWD
Center clone name: CH230-414K6
----- Summary Statistics -----
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 116547 bases at least Q40
Consensus quality: 124096 bases at least Q30
Consensus quality: 130590 bases at least Q20
Estimated insert size: 123351; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1025: contig of 1025 bp in length
* 1026 1125: gap of unknown length
* 1126 2392: contig of 1267 bp in length
* 2393 2492: gap of unknown length
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* 12632 12731: gap of unknown length
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* 55132 55231: gap of unknown length
* 55232 58148: contig of 2917 bp in length
* 58149 58248: gap of unknown length
* 58249 61446: contig of 3198 bp in length
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* 64495 64594: gap of unknown length
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* 69173 69272: gap of unknown length
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* 71998 75198: contig of 3201 bp in length
* 75199 75298: gap of unknown length
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* 78976 83527: contig of 4552 bp in length
* 83528 83627: gap of unknown length
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* 87338 87437: gap of unknown length
* 87438 91406: contig of 3968 bp in length
* 91406 91505: gap of unknown length
* 91506 94931: contig of 3426 bp in length
* 94932 95031: gap of unknown length
* 95032 99865: contig of 4834 bp in length
* 99866 99965: gap of unknown length
* 99966 104149: contig of 4184 bp in length
* 104150 104249: gap of unknown length
* 104250 108273: contig of 4024 bp in length
* 108274 108373: gap of unknown length

* 108374 113922: contig of 5549 bp in length
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Query Match 92.0%; Score 18.4; DB 2; Length 137930;
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTAAATGAGAGTGGCT 20
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Db 3994 GCAGTAAATGAGAGTGGCT 3975

RESULT 5
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LOCUS
DEFINITION
Rattus norvegicus clone CH230-141D21, *** SEQUENCING IN PROGRESS

AC114144
VERSION
AC114144.4 GI:30579617
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 217073)
Muzny, D., Marie, H., Metzker, M., Lee, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
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Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,
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Hollins, B., Howells, S., Hui, J., Hume, J., Idler, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensheva, L., Louisedge, H., Lozano, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
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Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
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Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 217073)
 Worley, K. C.
 Direct Submission
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 217073)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On May 13, 2003 this sequence version replaced gi:23110872.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GLNY
 Center clone name: CH230-141D21
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 196076 bases at least Q40
 Consensus quality: 198750 bases at least Q30
 Consensus quality: 200994 bases at least Q20
 Estimated insert size: 293933; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and the accession number will be preserved.
 * the accession number will be 217073 bp in length.

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 Query Match 92.0%; Score 18.4; DB 2; Length 217073;

Best Local Similarity 95.0%; Pred. No. 67;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGAGAGTGGCT 20
 |||||
 Db 39797 GCAGTTAATGAGAGTGGCT 39816
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 RESULT 6
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 DEFINITION
 Mus musculus chromosome 1, clone RP23-260K6, complete sequence.
 AC110250
 VERSION
 AC110250.16 GI:45917438
 KEYWORDS
 HTG.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren, B., Nusbaum, C. and Lander, E.
 1 (bases 1 to 219359)
 Mus musculus chromosome 1, clone RP23-260K6
 Unpublished
 2 (bases 1 to 219359)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Pettersen, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 219359)
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Liu, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ranasingh, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (28-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

[illegible]

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Query Match          92.0%; Score 18.4; DB 10; Length 219359;
Best Local Similarity 95.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
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LOCUS
DEFINITION
AB070355
VERSION
KEYWORDS
SOURCE
ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1
Miyake, Y., Nakamura, N., Matsushita, M., Tanaka, S., Inoue, H. and
Kanazawa, H.
rat kinesin-family protein, KIF1Bp204 isoform
Unpublished
2 (bases 1 to 6032)
Miyake, Y., Nakamura, N., Matsushita, M., Tanaka, S., Inoue, H. and
Kanazawa, H.
Direct Submission
Submitted (20-AUG-2001) Norihiro Nakamura, Osaka University, Dept.
of Biol., Grad. Sch. of Sci.; Machikaneyama, Toyonaka, Osaka
560-0032, Japan (E-mail: nnakamura@bio.sci.osaka-u.ac.jp,
Tel: 81-6-6850-5820, Fax: 81-6-6850-5817)
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DEFINITION
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AC100641
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 53722)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
2 (bases 1 to 53722)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckhalter, B.,
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Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIGR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15839
Center clone name: 162_D_22

* NOTE: This record contains 65 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone

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- * will be sequenced to completion. In the event that
- * the record is updated, the accession number will
- * be preserved.

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*	13263	13973:	contig	of 711	bp in length
*	13974	14073:	gap	of 100	bp
*	14074	14806:	contig	of 733	bp in length
*	14807	14906:	gap	of 100	bp
*	14907	15633:	contig	of 727	bp in length
*	15634	15733:	gap	of 100	bp
*	15734	16467:	contig	of 734	bp in length
*	16468	16567:	gap	of 100	bp
*	16568	17287:	contig	of 720	bp in length
*	17288	17387:	gap	of 100	bp
*	17388	18113:	contig	of 726	bp in length
*	18114	18213:	gap	of 100	bp
*	18214	19919:	contig	of 706	bp in length
*	19920	19019:	gap	of 100	bp
*	19020	19756:	contig	of 737	bp in length
*	19757	19856:	gap	of 100	bp
*	19857	20579:	contig	of 723	bp in length
*	20580	20679:	gap	of 100	bp
*	20680	21391:	contig	of 712	bp in length
*	21392	21491:	gap	of 100	bp
*	21492	22221:	contig	of 730	bp in length
*	22222	22321:	gap	of 100	bp
*	22322	23074:	contig	of 753	bp in length
*	23075	23174:	gap	of 100	bp
*	23175	23879:	contig	of 705	bp in length
*	23880	23979:	gap	of 100	bp
*	23980	24701:	contig	of 722	bp in length
*	24702	24801:	gap	of 100	bp
*	24802	25531:	contig	of 730	bp in length
*	25532	25631:	gap	of 100	bp
*	25632	26381:	contig	of 750	bp in length
*	26382	26481:	gap	of 100	bp
*	26482	27223:	contig	of 742	bp in length
*	27242	27323:	gap	of 100	bp
*	27324	28059:	contig	of 736	bp in length
*	28060	28159:	gap	of 100	bp
*	28160	28892:	contig	of 733	bp in length
*	28893	28992:	gap	of 100	bp

28993	29726:	contig	of 734	bp in length
29827	29826:	gap	of 100	bp
29827	29826:	contig	of 708	bp in length
30635	30634:	gap	of 100	bp
30635	31353:	contig	of 725	bp in length
31360	31459:	gap	of 100	bp
31460	32176:	contig	of 717	bp in length
32177	32276:	gap	of 100	bp
32277	32276:	contig	of 745	bp in length
33022	33121:	gap	of 100	bp
33122	33872:	contig	of 751	bp in length
33873	33972:	gap	of 100	bp
33973	34697:	contig	of 725	bp in length
34698	34797:	gap	of 100	bp
34798	35509:	contig	of 712	bp in length
35510	35609:	gap	of 100	bp
35610	36328:	contig	of 719	bp in length
36329	36428:	gap	of 100	bp
36429	37143:	contig	of 715	bp in length
37244	37243:	gap	of 100	bp
37244	37950:	contig	of 707	bp in length
37951	38050:	gap	of 100	bp
38051	38789:	contig	of 739	bp in length
38790	38889:	gap	of 100	bp
38890	39633:	contig	of 750	bp in length
39640	39739:	gap	of 100	bp
39740	40471:	contig	of 732	bp in length
40472	40571:	gap	of 100	bp
40572	41293:	contig	of 722	bp in length
41294	41393:	gap	of 100	bp
41394	42093:	contig	of 702	bp in length
42096	42193:	gap	of 100	bp
42196	42937:	contig	of 742	bp in length
42938	43037:	gap	of 100	bp
43038	43773:	contig	of 736	bp in length
43774	43877:	gap	of 100	bp
43874	44618:	contig	of 745	bp in length
44619	44718:	gap	of 100	bp
44719	45436:	contig	of 718	bp in length
45437	45536:	gap	of 100	bp
45537	46263:	contig	of 733	bp in length
46270	46369:	gap	of 100	bp
46370	47104:	contig	of 735	bp in length
47105	47204:	gap	of 100	bp
47205	47922:	contig	of 725	bp in length
47930	48029:	gap	of 100	bp
48030	48725:	contig	of 696	bp in length
48726	48825:	gap	of 100	bp
48826	49543:	contig	of 724	bp in length
49549	49649:	gap	of 100	bp
49650	50389:	contig	of 740	bp in length
50390	50489:	gap	of 100	bp
50490	51228:	contig	of 739	bp in length
51229	51326:	gap	of 100	bp
51329	52167:	gap	of 100	bp
52168	52909:	contig	of 742	bp in length
52910	53009:	gap	of 100	bp
53010	53722:	contig	of 713	bp in length

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
5. <i>Other</i>	
6. <i>Other</i>	
7. <i>Other</i>	
8. <i>Other</i>	
9. <i>Other</i>	
10. <i>Other</i>	
11. <i>Other</i>	
12. <i>Other</i>	
13. <i>Other</i>	
14. <i>Other</i>	
15. <i>Other</i>	
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17. <i>Other</i>	
18. <i>Other</i>	
19. <i>Other</i>	
20. <i>Other</i>	
21. <i>Other</i>	
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82. <i>Other</i>	
83. <i>Other</i>	
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99. <i>Other</i>	
100. <i>Other</i>	

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/mol_type="genomic DNA"  
/db_xref="taxon:10090"  
/clone="RP23-162D22"  
/clone_lib="RPCI-23 Fema
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ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 53722;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0;

1 GCAGTTAATGGAGAGTGCC 19

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Db      2188 GCAGTAATGGAGAGTGGC 2170
||||| ||||| ||||| ||||| |||||
RESULT 9
LOCUS   HS796F18      118968 bp      DNA      linear      PRI 04-MAR-2003
DEFINITION
Human DNA sequence from clone RP4-796F18 on chromosome
1p36.11-36.33, complete sequence.
ACCESSION
VERSION AL031291
KEYWORDS
SOURCE   HTG.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118968)
Direct Submission
Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 23, 1999 this sequence version replaced gi:4455618.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP4-796F18 is from the library RPCI-4 constructed by the group of
Pleier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.

FEATURES
Location/Qualifiers
1. ..118968
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="R2PD:RPCIP704F18796"
/db_xref="taxon:9606"
/chromosomes="1"
/map="p36.11-36.33"
/clone="RP4-796F18"
/clone_lib="RPCI-4"

ORIGIN
Query Match 87.0%; Score 17.4; DB 9; Length 118968;
Best Local Similarity 94.7%; Pred. No. 2.4e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 CAGTAATGGAGAGTGGCT 20

Db      28369 CAGATAATGGAGAGTGGCT 28387
||||| ||||| ||||| ||||| |||||
RESULT 10
LOCUS   AC118949/c
DEFINITION
Rattus norvegicus clone CH230-132J21, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
ACCESSION
VERSION AC118949.7 GI:25073628
KEYWORDS
SOURCE   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 153412)
Direct Submission
Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 23, 1999 this sequence version replaced gi:4455618.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP4-796F18 is from the library RPCI-4 constructed by the group of
Pleier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.

FEATURES
Location/Qualifiers
1. ..118968
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="R2PD:RPCIP704F18796"
/db_xref="taxon:9606"
/chromosomes="1"
/map="p36.11-36.33"
/clone="RP4-796F18"
/clone_lib="RPCI-4"

ORIGIN
Query Match 87.0%; Score 17.4; DB 9; Length 118968;
Best Local Similarity 94.7%; Pred. No. 2.4e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 CAGTAATGGAGAGTGGCT 20

```

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 153412)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Nov 19, 2002 this sequence version replaced gi:23194726.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUIA

Center clone name: CH230-132J21

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 136863 bases at least Q40

Consensus quality: 139024 bases at least Q30

Consensus quality: 140253 bases at least Q20

Estimated insert size: 138726; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 3815: contig of 3815 bp in length
 3816 3915: gap of unknown length
 3916 151370: contig of 147455 bp in length
 151371 151470: gap of unknown length
 151471 153412: contig of 1942 bp in length.

FEATURES

source
 1..153412
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-132J21"
 3916..5162
 misc_feature /note="wgs contig"
 55178..87575
 misc_feature /note="wgs_contig"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 153412;
 Best Local Similarity 94.7%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGTGGC 19

|||||

Db 77320 GCAGTTAATGGAGTGGC 77302

RESULT 11
 AL357135/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

AL357135 170847 bp DNA linear HTG 11-SEP-2001
 Homo sapiens chromosome 1 clone RP11-563B4, 21 unordered pieces.
 AL357135
 AL357135.4 GI:10186550
 HTG; HTGS_PHASE1; HTGS_CANCELLED.
 Homo sapiens
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Plumb.B.
 Direct Submission
 Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 Requests: clonerrequest@sanger.ac.uk
 On Sep 19, 2000 this sequence version replaced gi:10039951.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA563B4
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 164394 bases at least Q40
 Consensus quality: 166722 bases at least Q30
 Consensus quality: 168063 bases at least Q20
 Insert size: 168847; sum-of-contigs
 Insert size: 194310; 2.8% error; agarose-fp
 Quality coverage: 4.86x in Q20 bases; sum-of-contigs Quality
 coverage: 4.40x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 2836: contig of 2836 bp in length
 2837 2936: gap of 100 bp
 2937 10280: contig of 7344 bp in length
 10281 10380: gap of 100 bp
 10381 20606: contig of 10226 bp in length
 20607 20706: gap of 100 bp
 20707 24321: contig of 3615 bp in length
 24322 24421: gap of 100 bp
 24422 27351: contig of 2930 bp in length
 27352 34121: contig of 6670 bp in length
 34122 34221: gap of 100 bp
 34222 37457: contig of 3236 bp in length
 37458 37557: gap of 100 bp
 37558 50940: contig of 13383 bp in length
 50941 51040: gap of 100 bp
 51041 53739: contig of 2899 bp in length
 53740 53839: gap of 100 bp
 53840 60797: contig of 6958 bp in length
 60798 60897: gap of 100 bp
 60898 65168: contig of 4271 bp in length
 65169 65268: gap of 100 bp
 65269 75053: contig of 9785 bp in length
 75054 75153: gap of 100 bp
 75154 79444: contig of 4291 bp in length
 79445 84579: contig of 100 bp
 84580 84679: gap of 100 bp

	/note="assembly_fragment:01973 fragment_chain:4" 144551..164497
misc_feature	/note="assembly_fragment:00493" 164598..167306
misc_feature	/note="assembly_fragment:00496" 167407..170847
misc_feature	/note="assembly_fragment:01113 clone_end:SP6 vector_side:right"
ORIGIN	
Query Match	87.0% Score 17.4; DB 2;
Best Local Similarity	94.7% Pred.No.2.4e+02;
Matches 18; Conservative 0;	Mismatches 1
QY	2 CAGTAAATGGAGATGTCCT 20
Dd	126501 CAGATAATGGAGATGCT 126483
RESULT 12	
AC136550/c	
LOCUS	Rattus norvegicus clone CH230-195g2, ***
DEFINITION	***, 76 unordered pieces.
ACCESSION	AC136550
VERSION	AC136550.1 GI:24635348
KEYWORDS	HIG; HTGS_PHASE1.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; V Mammalia; Euthera; Rodentia; Sciurognath Rattus. 1 (bases 1 to 172869) Muzny,D.Marie., Metzker,M.Lee., Abramzon, Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Ba Baldwin,D., Bandaranaike,D., Barber,M., B Blawie,K., Blair,J., Blankenburg,K., Bly Bryant,N., Buhay,C., Burch,P., Burrell,K. Cardenas,V., Carter,K., Cavazos,I., Ceasa Chacko,J., Chavez,D., Chen,G., Chen,R., C Cleveland,C., Cockrell,R., Cox,C., Coyle, Davila,M.L., Davis,C., Davy-Carroll,L., D Delgado,O., Denison,S., Deramo,C., Ding,Y. Draper,H., Dugan-Rocha,S., Dunn,A., Durbi Egan,A., Escoto,M., Eugene,C., Evans,C.A Fernandez,S., Finley,M., Flagg,N., Forbes Fraser,C.M., Gabisi,A., Ganta,R., Garcia, Gueorgette,F., Geer,K., Gill,R., Grady, Gunaratne,P., Haaland,W., Hamill,C., Hamil Harvey,Y., Havlak,P., Hawes,A., Henderson Hernandez,R., Hines,S., Hladun,S.L., Hodg Hollins,B., Howells,S., Hulyk,S., Hume,J. Jackson,L., Jacob,L., Jiang,H., Johnson,B Karpathy,S., Kelly,S., Kelly,S., Khan,Z. Kowis,C., Kraft,C.L., Lebow,H., Leván,J., Liu,J., Liu,W., Liu,Y., London,P., Longac Loreshuwa,L., Louissegh,H., Lozadó,R.J. Maheshwari,M., Mahindartne,M., Mahmoud,M. Manung,B., Mapua,P.P., Martin,K., Martin,R. Mawney,S., McLeod,M., Monelli,T., Meene Miner,G., Minja,E., Montemayor,J., Moore,S Morris,S., Munidasa,M., Murphy,M., Nair,L Newton,N., Nguyen,N., Norris,S., Nwaokel Olarunpansoon,A., Pal,S., Parks,K., Pasto Peréz,A., Perez,L., Pfannkoch,C., Plopper Popovic,D., Primus,E., Pul-L., Puazo,M., Reeves,K., Regier,M.A., Reigh,R., Reilly,E Reuter,M., Richards,S., Riggs,F., Rives,C. Rose,M., Rose,R., Ruiz,S.J., Sanders,W., S Scott,G., Shatsman,S., Shen,H., Shetty,J. Shen,H., Shetty,J., Shetty,J., Shetty,J.

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Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R.,
Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 172869)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (06-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KDH
Center clone name: CH230-195G2
Center clone name: Summary Statistics
----- Sequencing Vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 100303 bases at least Q40
Consensus quality: 105648 bases at least Q30
Consensus quality: 109764 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1274 1273: contig of 1273 bp in length
1374 1373: gap of unknown length
2455 2455: contig of 1082 bp in length
2555 2555: gap of unknown length
3744 3744: contig of 1189 bp in length
3845 3845: gap of unknown length
5003 5003: contig of 1159 bp in length
5103 5103: gap of unknown length
5104 5104: contig of 1205 bp in length
6309 6309: gap of unknown length
6408 6408: contig of 1214 bp in length
7622 7622: gap of unknown length
7723 7723: contig of 1105 bp in length
8227 8227: gap of unknown length
8228 8228: gap of unknown length
8328 8328: gap of unknown length
10191 10191: contig of 1263 bp in length
10291 10291: gap of unknown length
11553 11553: contig of 1263 bp in length
11554 11554: gap of unknown length
11654 11654: contig of 1336 bp in length
12989 12989: gap of unknown length
13089 13089: contig of 1310 bp in length
14399 14399: gap of unknown length
14400 14400: gap of unknown length
14500 14500: contig of 1224 bp in length
15724 15724: gap of unknown length
15824 15824: contig of 1409 bp in length
17233 17233: gap of unknown length
17332 17332: contig of 1250 bp in length
18582 18582: gap of unknown length
18882 18882: gap of unknown length
20361 20361: contig of 1679 bp in length
20362 20461: gap of unknown length
20462 21520: contig of 1059 bp in length
21521 21620: gap of unknown length
21621 22023: contig of 1403 bp in length
23024 23123: gap of unknown length
23124 24409: contig of 1286 bp in length
24410 24509: gap of unknown length
24510 25677: contig of 1168 bp in length
25678 25777: gap of unknown length
25778 27162: contig of 1385 bp in length
27163 27262: gap of unknown length
27263 28658: contig of 1396 bp in length
28659 28758: gap of unknown length
28759 29923: contig of 1165 bp in length
29924 30023: gap of unknown length
30024 34288: contig of 1405 bp in length
31429 31528: gap of unknown length
31529 33308: contig of 1780 bp in length
33309 33408: gap of unknown length
33409 34620: contig of 1212 bp in length
34621 34720: gap of unknown length
34721 35820: contig of 1100 bp in length
35821 35920: gap of unknown length
35921 37668: contig of 1748 bp in length
37669 37768: gap of unknown length
37769 39648: contig of 1880 bp in length
39649 39748: gap of unknown length
39749 41500: contig of 1752 bp in length
41501 41600: gap of unknown length
41601 42994: contig of 1394 bp in length
42995 43094: gap of unknown length
43095 44591: contig of 1497 bp in length
44592 44692: gap of unknown length
44693 45799: contig of 1108 bp in length
45799 45899: gap of unknown length
45899 47714: contig of 1815 bp in length
47715 47815: gap of unknown length
47815 49419: contig of 1605 bp in length
49419 49519: gap of unknown length
49520 50983: contig of 1464 bp in length
50984 51083: gap of unknown length
51084 53133: contig of 2230 bp in length
53134 53414: gap of unknown length
53414 55701: contig of 2288 bp in length
55701 55801: gap of unknown length
55801 57807: contig of 2005 bp in length
57807 57906: gap of unknown length
57907 59877: contig of 1971 bp in length
59878 59977: gap of unknown length
59978 61331: contig of 1354 bp in length
61332 61431: gap of unknown length
61432 62734: gap of unknown length
62734 64694: contig of 1861 bp in length
64695 64794: gap of unknown length
64795 67383: contig of 2589 bp in length
67384 67483: gap of unknown length
67484 69848: contig of 2365 bp in length
69849 71378: gap of unknown length
71379 71478: gap of unknown length
71479 74107: contig of 2629 bp in length
74108 74207: gap of unknown length
74208 75991: contig of 1784 bp in length
75992 76091: gap of unknown length
76092 79225: contig of 3134 bp in length
79226 79325: gap of unknown length
79326 81701: contig of 2375 bp in length
81701 81800: gap of unknown length
81801 84427: contig of 2627 bp in length
84428 84528: gap of unknown length
84529 87905: contig of 3378 bp in length
87906 88005: gap of unknown length

* 88006 89848: contig of 1843 bp in length
 * 89849 89948: gap of unknown length
 * 91836: contig of 1888 bp in length
 * 91837 91936: gap of unknown length

Query Match 87.0%; Score 17.4; DB 2; Length 172869;
 Best Local Similarity 94.7%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCAGTAAATCGAGAGTGGC 19

Db 60256 GCAGTAAATCGAGAGTGGC 60238

RESULT 13

LOCUS AC135710 217844 bp DNA linear HTG 10-MAY-2003
 DEFINITION Rattus norvegicus clone CH230-136B24, WORKING DRAFT SEQUENCE.
 ACCESSION AC135710
 VERSION AC135710.3 GI:30520568
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 217844)

Muzny, D. Marie., Mettaker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, X., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Gant, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Haviak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louisleged, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoeleneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poidexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rokey, I., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smafs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, R., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 217844)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (21-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 217844)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

REFERENCE

AUTHORS
 TITLE
 JOURNAL

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GP12

Center clone name: CH230-136B24

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 206180 bases at least Q40

Consensus quality: 207708 bases at least Q30

Consensus quality: 208525 bases at least Q20

Estimated insert size: 215272; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 217844: contig of 217844 bp in length.

FEATURES

source

1. 217844

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-136B24"

1. 1699

/note="wgs contig"

215317. 217844

/note="wgs_contig"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 217844;

Best Local Similarity 94.7%; Pred. No. 2.3e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2  CAGTTAATGGAGAGTGGCT 20
Db      119616  CAGTTAATGGAGAGTGGCT 119634

RESULT 14
AC133519/c
LOCUS   Mus musculus chromosome 5 clone RP23-178N9, WORKING DRAFT SEQUENCE,
DEFINITION 6 unordered pieces.
ACCESSION AC133519
VERSION   AC133519.2 GI:48475388
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE    Mus musculus
ORGANISM  Mus musculus (house mouse)

REFERENCE
AUTHORS   Wilson,R.K.
TITLE     The sequence of Mus musculus clone
JOURNAL   Unpublished
2 (bases 1 to 220270)
REFERENCE McPherson,J.D. and Waterston,R.H.
AUTHORS   Direct Submission
JOURNAL   Submitted (13-SEP-2002) Genome Sequencing Center, 4444 Forest Park
          Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 220270)
REFERENCE Wilson,R.K.
AUTHORS   Direct Submission
JOURNAL   Submitted (09-JUN-2004) Genome Sequencing Center, 4444 Forest Park
          Parkway, St. Louis, MO 63108, USA
COMMENT   On Jun 9, 2004 this sequence version replaced gi:22830511.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0178N08
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 218635 bases at least Q40
Consensus quality: 219029 bases at least Q30
Consensus quality: 219205 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2442: contig of 2442 bp in length
* 2443 2342: gap of unknown length
* 2543 8496: contig of 5954 bp in length
* 8497 8596: gap of unknown length
* 8597 27383: contig of 18787 bp in length
* 27384 27483: gap of unknown length
* 27484 41118: contig of 13635 bp in length
* 41119 41218: gap of unknown length
* 41219 123323: contig of 82105 bp in length
* 123324 123423: gap of unknown length
* 123424 220270: contig of 96847 bp in length.
          Location/Qualifiers
          1..220270

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
/clone="RP23-178N9"
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/feature="assembly_name:Contig11"
2543..8496
/feature="assembly_name:Contig12"
8597..27383
/feature="assembly_name:Contig13"
27484..41118
/feature="assembly_name:Contig14"
41219..123323
/feature="assembly_name:Contig15"
123424..220270
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misc_feature
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misc_feature
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misc_feature

ORIGIN
Query Match 87.0%; Score 17.4; DB 2; Length 220270;
Best Local Similarity 94.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCAGTTAATGGAGAGTGGC 19
Db      111496  GCAGTTAATGGAGAGTGGC 111478

RESULT 15
AC229361
LOCUS   Rattus norvegicus clone CH230-132Pl4, *** SEQUENCING IN PROGRESS
DEFINITION *** 10 unordered pieces.
ACCESSION AC229361
VERSION   AC229361.5 GI:25138171
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 252428)
AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
          Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
          Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
          Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
          Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
          Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
          Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
          Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
          Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
          Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
          Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
          Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
          Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
          Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
          Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
          Gebregeorgis,E., Geek,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
          Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
          Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
          Hernandez,R., Hines,S., Hlucun,S.L., Hodgson,A., Hogues,M.,
          Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
          Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
          Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
          Kowis,C., Kraft,C.I., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
          Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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          Maheshwari,M., Mahindartne,N., Mahmoud,M., Malloy,K., Mangum,A.,
          Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
          Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
          Milosavljevic,A., Minter,G., Minja,E., Montemayor,J., Moore,S.,
          Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
          Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,

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Nwaoketeme, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puaro, B., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, M., Reilly, M., Ren, X., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlecyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .252428

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-132P14"

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22161. .23454

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27044. .28504

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28605. .29988

/note="wgs_contig"

104489. .106119

/note="wgs_contig"

140217. .141056

/note="clone_boundary"

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end_sequence:BH322645"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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0;

0;

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0;

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0;

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0;

0;

0;

0;

0;

0;

0;

* 18381 22060: contig of 3680 bp in length
 * 22061 22160: gap of unknown length
 * 22161 28504: contig of 6344 bp in length
 * 28505 28604: gap of unknown length
 * 28605 58561: contig of 29957 bp in length
 * 58562 58661: gap of unknown length
 * 58662 73066: contig of 14405 bp in length
 * 73067 73166: gap of unknown length
 * 73167 93446: contig of 20280 bp in length
 * 93447 93547: gap of unknown length
 * 93548 106119: contig of 12573 bp in length
 * 106120 247882: contig of 141663 bp in length
 * 247883 247982: gap of unknown length
 * 247983 249383: contig of 1401 bp in length
 * 249384 252428: gap of unknown length
 * 252429 252428: contig of 2945 bp in length.

Location/Qualifiers

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/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-132P14"

1. .2012

/note="wgs_end_extension"

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2096. .2942

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clone_end:Sp6"

site:

end_sequence:BH322647"

18381. .19898

/note="wgs_contig"

22161. .23454

/note="wgs_contig"

27044. .28504

/note="wgs_contig"

28605. .29988

/note="wgs_contig"

104489. .106119

/note="wgs_contig"

140217. .141056

/note="clone_boundary"

clone_end:17"

end_sequence:BH322645"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

***** Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ***** Project Information
 Center project name: GULB
 Center clone name: CH230-132P14
 ***** Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 198733 bases at least Q40
 Consensus quality: 203216 bases at least Q30
 Consensus quality: 206587 bases at least Q20
 Estimated insert size: 191466; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 18280: contig of 18280 bp in length
 * 18281 19380: gap of unknown length

* 18381 22060: contig of 3680 bp in length
 * 22061 22160: gap of unknown length
 * 22161 28504: contig of 6344 bp in length
 * 28505 28604: gap of unknown length
 * 28605 58561: contig of 29957 bp in length
 * 58562 58661: gap of unknown length
 * 58662 73066: contig of 14405 bp in length
 * 73067 73166: gap of unknown length
 * 73167 93446: contig of 20280 bp in length
 * 93447 93547: gap of unknown length
 * 93548 106119: contig of 12573 bp in length
 * 106120 247882: contig of 141663 bp in length
 * 247883 247982: gap of unknown length
 * 247983 249383: contig of 1401 bp in length
 * 249384 252428: gap of unknown length
 * 252429 252428: contig of 2945 bp in length.

 ACCESSION AC097422
 VERSION AC097422.6 GI:30521339
 KEYWORDS HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 252630)
 AUTHORS Murthy D.Maris., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguliano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calgeron, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinu, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Ganta, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Hawlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Labow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuwa, L., Louleseg, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokeneme, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.L., Puazo, K., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savory, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villanar, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlecyk, R., Wooden, H., Worley, K., Wright, D., Wright, J., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (18-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252630)
Rat Genome Sequencing Consortium.
Direct Submission
2 (bases 1 to 252630)
Worley, K.C.

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 10, 2003 this sequence version replaced gi:23265371.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature

table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIGB
Center clone name: CH230-20B11
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 230655 bases at least Q40
Consensus quality: 233238 bases at least Q30
Consensus quality: 235484 bases at least Q20
Estimated insert size: 248907; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbankdraftdata.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 246059: contig of 246059 bp in length
* 246060 246159: Gap of unknown length
* 246160 249026: contig of 2867 bp in length
* 249027 249126: gap of unknown length
* 249127 252630: contig of 3504 bp in length.

FEATURES
source

1..252630
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-20B11"

misc_feature

1..1962
/note="wgs_end_extension
clone_end:T7"
complement(8851..9686)
/note="clone_boundary
clone_end:T7"
site:EcoRI
end_sequence:BH317725"

misc_feature

210372..210481
/note="clone_boundary
clone_end:Sp6
site:EcoRI
end_sequence:BH317726"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 252630;
Best Local Similarity 94.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGC 19
|||||

Db 2333S8 GCAGTTAATGGACAGTGGC 233340
|||||

RESULT 17

AC123476/c

LOCUS

DEFINITION

AC123476

VERSION

KEYWORDS

SOURCE

ORGANISM

AC123476 286008 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-54E17, *** SEQUENCING IN PROGRESS
***, 8 unordered pieces.

AC123476 GI:25137780

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 286008)
 Muzny, D. Marie, Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gebregregis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
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 Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
 Sanders, J., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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 Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhauser, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstein, G., and Gibbs, R. A.
 Direct Submission
 2 (bases 1 to 286008)
 Worley, K. C.
 Direct Submission
 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 286008)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 20, 2002 this sequence version replaced gi:23267686.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information
 Center project name: GX0A
 Center clone name: CH230-54E17

----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 256108 bases at least Q40
 Consensus quality: 258933 bases at least Q30
 Consensus quality: 260818 bases at least Q20

 Estimated insert size: 257835; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * NOTE: This sequence may represent more than one 'Clone-
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 3047: contig of 3047 bp in length
 * 3048 3147: gap of unknown length
 * 3148 6454: contig of 3307 bp in length
 * 6455 6554: gap of unknown length
 * 6555 29749: contig of 23195 bp in length
 * 29750 29849: gap of unknown length
 * 29850 36849: contig of 7000 bp in length
 * 36850 36949: gap of unknown length
 * 36950 281641: contig of 244692 bp in length
 * 281642 281741: gap of unknown length
 * 281742 282750: contig of 1009 bp in length
 * 282751 282850: gap of unknown length
 * 282851 284480: contig of 1630 bp in length
 * 284481 284580: gap of unknown length
 * 284581 286008: contig of 1428 bp in length.

FEATURES

1. 286008
 /organism="Rattus norvegicus"

/mol_type="Genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-54E17"

5. 452

/note="clone boundary"

clone_end:77

site:

end_sequence:BH347016"

1988..3047

/note="wgs contig"

6555..8218

/note="wgs contig"

18278..20497

/note="wgs contig"

29850..31190

/note="wgs contig"

complement(241566..242265)

/note="clone boundary"

clone_end:Sp6

site:

end_sequence:BH347018"

ORIGIN

Query Match 87.0%; Score 17.4; DB 2; Length 286008;
Best Local Similarity 94.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGGCT 20
|||||
Db 55471 CAGTTAATGGAGAGTGGCT 55453
|||||

RESULT 18
G86517/c
LOCUS
DEFINITION S209P6502FD2.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged
G86517 578 bp DNA linear STS 06-SEP-2002
ACCESSION S209P6502FD2.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged
VERSION G86517
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Wade, C.
TITLE Polymorphism Structure in the Mouse
JOURNAL Unpublished (2002)
COMMENT Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172512177
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 578

Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated
as STS and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.

FEATURES
source
Location/Qualifiers
1..578
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C3H/HeJ"
/db_xref="taxon:10090"
/map="10 22-530 11816210-11816717"
/clone_lib="C3H/HeJ"
<1..>578

STS
ORIGIN
Query Match 85.0%; Score 17; DB 11; Length 578;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAATGGAGAGTGGCT 20
|||||
Db 261 GTTAATGGAGAGTGGCT 245
|||||

RESULT 19
AK119449
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-133-D06, full
insert sequence.
ACCESSION AK119449
VERSION AK119449.1 GI:37989072

KEYWORDS
SOURCE ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
COMMENT

FLI CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Naniwa, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Chen, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otomoto, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Teunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ootani, N., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayaishizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764
2
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hayashizaki, T., Hata, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoaka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Kikuchi, S.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y.,
Nakamura, M., Naniwa, T., Narikawa, R., Niikura, J., Nishi, K.,
Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M.,
Ooka, H., Ootani, N., Ota, Y., Otomoto, Y., Ryu, R., Satoh, K., Sakai, C.,
Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Hotta, I.,
Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y.,
Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M.,
Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K.,
Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S. and Yoshimura, A.
Collection, mapping, and annotation of 28K full-length cDNA clones
from japonica rice
Unpublished
3 (bases 1 to 3449)
Kikuchi, S.
Direct Submission
Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
rice.
UPL : http://cdna01.dna.affrc.go.jp/cdna/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Naniwa, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Otomoto, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M.,
Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,

```

Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hikamoto,K.,
Hiroaka,T., Hori,P., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kaga,A., Kanagawa,S., Kato,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurinara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K.,
Shinagawa,A., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,E.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
1. 3449
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="rRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-133-D06"

FEATURES
             source
Query Match      85.0%; Score 17; DB 8; Length 3449;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAGTTAATGGAGAGTGG 18
DB 2292 CAGTTAATGGAGAGTGG 2308

RESULT 20
AC131074/c
LOCUS
DEFINITION Mus musculus clone RP23-405M12, WORKING DRAFT SEQUENCE, 23
unordered pieces.
ACCESSION AC131074
VERSION AC131074.3 GI:30017737
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 53724)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-405M12
Unpublished
2 (bases 1 to 53724)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faroo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,B., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M.,
McCarthy,M., Melidrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 53724)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Atchchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Faro,S.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faroo,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,B., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tefaye,S., Theodore,J., Topham,K., Travers,M., Stubbs,M.,
Talamas,J., Tefaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:27753724.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26991
Center clone name: 405_M_12
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1053: contig of 1053 bp in length
* 1054: gap of 100 bp
* 1153: contig of 100 bp
* 1154: gap of 100 bp
* 1885: contig of 732 bp in length
* 1886: gap of 100 bp
* 1986: contig of 1280 bp in length
* 3265: gap of 100 bp
* 3266: contig of 890 bp in length
* 4255: contig of 100 bp
* 4355: gap of 100 bp
* 5319: contig of 964 bp in length
* 5320: gap of 100 bp
* 5420: contig of 1554 bp in length
* 6974: gap of 100 bp
* 7074: contig of 996 bp in length
* 8070: gap of 100 bp
* 8170: contig of 1010 bp in length
* 9180: gap of 100 bp
* 9280: contig of 13080 bp in length
* 22360: gap of 100 bp
* 22460: contig of 1192 bp in length
* 23652: gap of 100 bp
* 23752: contig of 1595 bp in length
* 25347: gap of 100 bp
* 25446: contig of 469 bp in length
* 25915: gap of 100 bp
* 26016: contig of 1144 bp in length
* 27159: gap of 100 bp
* 28219: contig of 960 bp in length

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ORIGIN

Query Match 85.0%; Score 17; DB 5; Length 177660;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CAGTTAATGGAGAGTGG 18
 |||||
 Db 7174 CAGTTAATGGAGAGTGG 7158

RESULT 22

AC108432 178061 bp DNA linear HTG 11-AUG-2004
 Mus musculus chromosome 7 clone RP23-170D4 map 7, *** SEQUENCING IN
 PROGRESS *** 9 unordered pieces.

ACCESSION

AC108432

HTG; HTGS_PHASE1; HTGS_FULTOP; HTGS_ACTIVEFIN.

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 178061)
 Birren, B., Nusbaum, C. and Lander, E.

Mus musculus chromosome 7, clone RP23-170D4

2 (bases 1 to 178061)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Canarata, J., Campiano, A., Chang, J., Chararo, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kellis, C., LaRocque, K., Lamazares, R.,

Landers, T., Lechoczky, J., Levine, R., Liu, G., MacLean, C.,

Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,

McSwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,

Ming, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,

Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,

Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,

Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 178061)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,

Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J.,

Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,

Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,

Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,

Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R.,

MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,

McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V.,

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,

O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, J., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R.,

Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,

TITLE

JOURNAL

COMMENT

Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (11-AUG-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 11, 2004 this sequence version replaced gi:49658801.
 All repeats were identified using RepeatMasker:
 Smit, A. F. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RN/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@broad.mit.edu
 ----- Project Information
 Center project name: L20748
 Center clone name: 170_D_4

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 17256: contig of 17256 bp in length
 * 17257 17356: gap of unknown length
 * 17357 29522: contig of 12166 bp in length
 * 29523 29622: gap of unknown length
 * 29623 56808: contig of 27186 bp in length
 * 56809 56908: gap of unknown length
 * 56909 96993: contig of 39985 bp in length
 * 96994 101710: gap of unknown length
 * 101711 101810: contig of 4717 bp in length
 * 101811 114309: contig of 12499 bp in length
 * 114310 114409: gap of unknown length
 * 114410 150584: contig of 36175 bp in length
 * 150585 150684: gap of unknown length
 * 150685 174736: contig of 24052 bp in length
 * 174737 174836: gap of unknown length
 * 174837 178061: contig of 3225 bp in length.

FEATURES

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 /clone_lib="RPCI-23 Female Mouse BAC"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAAATGGAGAGTGGCT 20

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 Db 110346 GTTAAATGGAGAGTGGCT 110362

RESULT 23

HS435D1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

HS435D1 184975 bp DNA linear PRI 07-AUG-2003
 Human DNA sequence from clone RP3-435D1 on chromosome Xq25,
 complete sequence.
 ACCESSION Z86064
 VERSION Z86064.2 GI:33504457
 KEYWORDS HTG
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 184975)
TITLE	Bird.C.
JOURNAL	Direct Submission
COMMENT	Submitted (07-AUG-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk On Aug 7, 2003 this sequence version replaced gi:3191972. ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk ----- During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C-elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP3-435D1 is from the library RP3-3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2.
FEATURES	Location/Qualifiers 1..184975 /organism="Homo sapiens" /mol_type="Genomic DNA" /db_xref="RZPD:RPCIP704D01435" /db_xref="taxon:9606" /chromosome="X" /map="Q25" /clone="RP3-435D1" /clone_lib="RP3-3"
ORIGIN	Query Match 85.0%; Score 17; DB 9; Length 184975; Best Local Similarity 100.0%; Pred.No. 3.9e+02; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 3 AGTTAATCGAGATGGC 19 Db 92839 AGTTAATCGAGATGGC 92855 RESULT 24 AC046179 208657 bp DNA linear HTG 05-SEP-2000 LOCUS DEFINITION Homo sapiens chromosome X clone RP11-789M2 map X, WORKING DRAFT SEQUENCE, 23 unordered pieces. AC046179 ACCESSION AC046179 KEYWORDS AC046179.3 GI:9966987 HTGS_PHASE1; HTGS_DRAFT. SOURCE Homo sapiens (human) ORGANISM Homo Sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 208657)
TITLE	Birren,B., Linton,L., Nussbaum,C., Lander,E., Abraham,H., Allen,N., Andersson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,D., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., GrandPierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Labrecque,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marguis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Navlor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
JOURNAL	Direct Submission
COMMENT	Submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 5, 2000 this sequence version replaced gi:8569193. All repeats were identified using RepeatMasker: Smit,A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L9613 Center clone name: 789_M2 ----- Summary Statistics Sequencing vector: M13; M77815; 97% of reads Sequencing vector: Plasmid; n/a; %0.f% of reads 2.844066688450288Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 195307 bases at least Q40 Consensus quality: 201602 bases at least Q30 Consensus quality: 204197 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 206457; sum-of-contigs Quality coverage: 8.2 in Q20 bases; agarose-fp Quality cov. * NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 1 144: contig of 144 bp in length * 145 244: gap of 100 bp * 245 1319: contig of 1075 bp in length * 1320 1419: gap of 100 bp * 1420 2798: contig of 1379 bp in length * 2799 2898: gap of 100 bp * 2899 3998: contig of 1100 bp in length * 3999 4099: gap of 100 bp * 4099 5245: contig of 1147 bp in length

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* 5246 5345: gap of 100 bp
* 5346 7038: contig of 1693 bp in length
* 7039 7138: gap of 100 bp
* 7139 8266: contig of 1128 bp in length
* 8267 8366: gap of 100 bp
* 8367 9973: contig of 1507 bp in length
* 9974 10073: gap of 100 bp
* 10074 11264: contig of 1191 bp in length
* 11265 11364: gap of 100 bp
* 11365 12770: contig of 1406 bp in length
* 12771 12870: gap of 100 bp
* 12871 14971: contig of 2101 bp in length
* 14972 15071: gap of 100 bp
* 15072 16413: contig of 1342 bp in length
* 16414 16513: gap of 100 bp
* 16514 18132: contig of 1619 bp in length
* 18133 18232: gap of 100 bp
* 18233 19846: contig of 1614 bp in length
* 19847 19946: gap of 100 bp
* 19947 21603: contig of 1657 bp in length
* 21604 21703: gap of 100 bp
* 21704 23300: contig of 1597 bp in length
* 23301 24401: gap of 100 bp
* 24402 24501: contig of 1001 bp in length
* 24502 24502: gap of 100 bp
* 24502 94227: contig of 69726 bp in length
* 94228 94327: gap of 100 bp
* 94328 102811: contig of 8484 bp in length
* 102812 102911: gap of 100 bp
* 102912 118842: contig of 15931 bp in length
* 118843 118942: gap of 100 bp
* 118943 163248: contig of 44306 bp in length
* 163249 163348: gap of 100 bp
* 163349 205638: contig of 42290 bp in length
* 205639 205738: gap of 100 bp
* 205739 208657: contig of 2919 bp in length.
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="X"
            /map="X"
            /clone="RP11-789M2"
            /clone_lib="RPC1-11 Human Male BAC"
        1..144
            /note="assembly_fragment
            clone_end:SP6
            vector_side:left"
        245..1319
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        1420..2798
            /note="assembly_fragment"
        2899..3998
            /note="assembly_fragment"
        4099..5245
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        11365..12770
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misc_feature 118943..163248
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              /note="assembly_fragment"
misc_feature 205739..208657
              /note="assembly_fragment
              clone_end:17
              vector_side:right"
ORIGIN
Query Match      85.0%; Score 17; DB 2; Length 208657;
Best Local Similarity 100.0%; Pred.No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 ACTTAATGAGAGTGGC 19
        |||||
Db      184476 ACTTAATGAGAGTGGC 184492

RESULT 25
AC093316      226567 bp      DNA      linear      ROD 14-NOV-2002
LOCUS      Mus musculus chromosome 10 clone rp23-20217 strain C57BL/6J,
DEFINITION      complete sequence.
ACCESSION      AC093316
VERSION      AC093316.28 GI:24961383
KEYWORDS      HTG.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      1 (bases 1 to 226567)
JOURNAL      Mus musculus Chromosome 10 BAC Clone rp23-20217
REFERENCE
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      2 (bases 1 to 226567)
JOURNAL      Direct Submission
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (17-AUG-2001) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
REFERENCE
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      3 (bases 1 to 226567)
JOURNAL      Direct Submission
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (17-SEP-2002) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
REFERENCE
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      4 (bases 1 to 226567)
JOURNAL      Direct Submission
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (27-SEP-2002) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA
REFERENCE
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      5 (bases 1 to 226567)
JOURNAL      Direct Submission
AUTHORS      Zhou,L., Fu,Y. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (22-OCT-2002) Department Of Chemistry And Biochemistry,
              The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
              OK 73019, USA

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REFERENCE
AUTHORS
TITLE
JOURNAL
6 (bases 1 to 226567)
Zhou,L., Fu,Y. and Roe,B.A.
Direct Submission
Submitted (23-OCT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
7 (bases 1 to 226567)
Zhou,L., Fu,Y. and Roe,B.A.
Direct Submission
Submitted (14-NOV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT
On Nov 14, 2002 this sequence version replaced gi:24211257.
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Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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/notes="This is one of two clones in the same well from
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Query Match 85.0%; Score 17; DB 10; Length 226567;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTTAATGGAGAGTGCT 20
|||||
Db 138639 GTTAATGGAGAGTGCT 138655
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RESULT 26
AC127933/6
LOCUS
DEFINITION
Rattus norvegicus clone CH230-180F1, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
ACCESSION
AC127933
VERSION
AC127933.2 GI:22856130
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS
1 (bases 1 to 232203)
Murny,D.Marie., Metker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Jackson,J., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Minet,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K.,
Nwackemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
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Puato,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Shen,H.,
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Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
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Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,S., Villalana,B., Waldron,L., Walker,B., Wang,J.,
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Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 232203)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 232203)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21908462.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
-----
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----
Project Information
Center project name: GXVP
Center clone name: CH230-180F1
-----
Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 208067 bases at least Q40
Consensus quality: 210828 bases at least Q30
Consensus quality: 212578 bases at least Q20
Estimated insert size: 228129; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----

```

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 205148: contig of 205148 bp in length
 * 205149 205248: gap of unknown length
 * 205249 206326: contig of 1078 bp in length
 * 206327 206426: gap of unknown length
 * 206427 232203: contig of 25777 bp in length.
 * Location/Qualifiers
 * 1..232203
 * /organism="Rattus norvegicus"
 * /mol_type="genomic DNA"
 * /db_xref="taxon:10116"
 * /clone="CH230-180F1"

FEATURES

source

ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 232203;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AGTTAATGAGAGTGCG 19
 Db 31862 AGTTAATGAGAGTGCG 31846
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RESULT 27

AC103284

LOCUS

DEFINITION

Rattus norvegicus clone CH230-125L23, WORKING DRAFT SEQUENCE, 4

ACCESSION

AC103284.5 GI:30579046

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULUTOP.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 247342)

REFERENCE

AUTHORS

Murny,D,Marie., Metzker,M, Lee., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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 Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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 Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J.,
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 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C.U., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, N., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
 Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Shen, H.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, J.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
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 Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
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 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 247342)

Worley, K.C.

Direct Submission

Submitted (24-NOV-2001)

Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 247342)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003)

Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23269025.

The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GJ51

Center Clone name: CH230-125L23

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 230773 bases at least Q40

Consensus quality: 234024 bases at least Q30

Consensus quality: 236028 bases at least Q20

Estimated insert size: 243299; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence

* as soon as it is available and the accession number will
* be preserved.

* 1 242486: contig of 242486 bp in length
* 242487 242586: gap of unknown length
* 242587 243832: contig of 1246 bp in length
* 243833 245280: gap of unknown length
* 243933 245280: contig of 1348 bp in length
* 245281 245380: gap of unknown length
* 245381 247342: contig of 1962 bp in length.

FEATURES

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1. 247342
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-125L23"
misc_feature
1. 2566
/note="wgs_contig"

ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 247342;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAATGCAGAGTGGCT 20

Db 149558 GTTAATGCAGAGTGGCT 149574

RESULT 28

AC111661/c

LOCUS Rattus norvegicus clone CH230-246A22, WORKING DRAFT SEQUENCE. linear HTG 15-NOV-2002

DEFINITION Rattus norvegicus clone CH230-246A22, WORKING DRAFT SEQUENCE.

AC111661

AC111661.4 G1:25007472

HTG; HTGS PHASR2; HTGS DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

SOURCE

ORGANISM
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 247649)

Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
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Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Jolivet,A.,
Jarkpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenshehwa,B., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Jolivet,A.,
Mangum,A., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaakemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,

FEATURES

Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Vilas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlarczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 247649)
Worley,K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 247649)
Rat Genome Sequencing Consortium.
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced g1:23603922.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMJR
Center clone name: CH230-246A22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 235200 bases at least Q40
Consensus quality: 238056 bases at least Q30
Consensus quality: 240059 bases at least Q20
Estimated insert size: 246501; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 247649: contig of 247649 bp in length.
Location/Qualifiers

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source
1. 247649
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/cclone="CH230-246A22"
misc_feature
1. 1531
/note="wgs_end_extension"
clone_end:T7"
misc_feature
2471..3153
/note="clone_boundary"
clone_end:T7"
site:
end_sequence:BZ164876"
misc_feature
complement(24753..247592)
/note="clone_boundary"
clone_end:Sp6
site:
end_sequence:BZ164877"

ORIGIN
Query Match 85.0%; Score 17; DB 2; Length 247649;
Best Local Similarity 100.0%; Pred.No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAATGGAGAGTGCT 20
|||||
Db 246986 GTTAATGGAGAGTGCT 246970

RESULT 29
AC126699/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-3M21, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC126699
AC126699.4 GI:30466861
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 267852)
Muzny D, Marie, Metzker, M.Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Evans, C., Evans, C.A., Falls, I., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hughes, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, B., Jacob, S., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpthy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuwa, L., Loulseg, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Napua, P., Martin, K., Martin, R., Martinez, E.,
Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nait, L.,

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Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokeme, O., Okwionu, G., Olarpunsgoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
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Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
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Valas, R., Vera, V., Villasana, B., Waldron, L., Walker, B., Wang, J.,
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Williams, G., Willson, R., Wleciyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 267852)
Worley, K.C.
Direct Submission
Submitted (09-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 267852)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24918314.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBST
Center clone name: CH230-3M21
----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 243899 bases at least Q40
Consensus quality: 246985 bases at least Q30
Consensus quality: 249301 bases at least Q20
Estimated insert size: 252851; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1 265123: contig of 265123 bp in length
* 265124 265223: gap of unknown length
* 265224 266991: contig of 1468 bp in length
* 266992 266991: gap of unknown length
* 266792 267852: contig of 1061 bp in length.
FEATURES
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            /db_xref="taxon:10116"
            /clone="CH230-3N21"
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            /note="wgs_contig"
        1974..5323
            /note="wgs_contig"
        191366..193020
            /note="wgs_contig"
        263978..265123
            /note="wgs_contig"
ORIGIN
Query Match      85.0%; Score 17; DB 2; Length 267852;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTTAATGGAGAGTGCT 20
Db 92518 GTTAATGGAGAGTGCT 92502

RESULT 30
AC122661 270720 bp DNA linear HTG 13-MAY-2003
LOCUS Rattus norvegicus clone CH230-239E4, WORKING DRAFT SEQUENCE, 5
DEFINITION
unordered pieces.
AC122661
AC122661.4 GI:30581467
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 270720)
Muzny,D,Marie, Metzker,M, Lee, Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Royagi,A., Avodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,X., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Georgievski,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,K., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hughes,M.,
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Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowals,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuwa,L., Loulsegheh,H., Lozada,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,

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Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwakoemei,O., Okwuonu,G., Olarunpungoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smalls,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valdes,R., Vera,V., Villanana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 270720)
Worley,K.C.
Direct Submission
Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 270720)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:22857158.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKJW
Center clone name: CH230-239E4
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 25292 bases at least Q40
Consensus quality: 23204 bases at least Q30
Consensus quality: 23376 bases at least Q20
Estimated insert size: 239318; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 263852: contig of 263852 bp in length
* 263853 263952: gap of unknown length
* 263953 265443: contig of 1291 bp in length
* 265444 265943: gap of unknown length
* 265944 267058: contig of 1715 bp in length
* 267059 267158: gap of unknown length
* 267159 268587: contig of 1429 bp in length
* 268588 268687: gap of unknown length
* 268688 270720: contig of 2033 bp in length.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-239E4"
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            misc_feature
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ORIGIN
    Query Match      85.0%; Score 17; DB 2: Length 270720;
    Best Local Similarity 100.0%; Pred. No. 3.9e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTTAATGGAGAGTGCT 20
|||||
Db 171218 GTTAATGGAGAGTGCT 171234

RESULT 31
AC102634
LOCUS AC102634 274998 bp DNA linear HTG 20-FEB-2004
DEFINITION Mus musculus chromosome 10 clone RP23-39C23 map 10, *** SEQUENCING
IN PROGRESS ***, 10 unordered pieces.
ACCESSION AC102634
VERSION AC102634.4 GI:42716204
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Biren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 10, clone RP23-39C23
Unpublished
2 (bases 1 to 274998)
Barren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
McLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,J., Retta,R., Riback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 274998)
Biren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,

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Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-FEB-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 20, 2004 this sequence version replaced GI:31455723.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19139
Center clone name: 39_C23

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 23017: contig of 23017 bp in length
* 23018 23117: gap of 100 bp
* 23118 53875: contig of 30758 bp in length
* 53876 53975: gap of 100 bp
* 53976 57492: contig of 3517 bp in length
* 57493 57592: gap of 100 bp
* 57593 77209: contig of 19617 bp in length
* 77210 81881: contig of 4572 bp in length
* 81882 81981: gap of 100 bp
* 81982 125097: contig of 43116 bp in length
* 125098 125197: gap of 100 bp
* 125198 164958: contig of 39761 bp in length
* 164959 165058: gap of 100 bp
* 165059 180062: contig of 15004 bp in length
* 180063 180162: gap of 100 bp
* 180163 221929: contig of 41767 bp in length
* 221930 222029: gap of 100 bp
* 222030 274998: contig of 52969 bp in length.
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            /mol_type="genomic DNA"
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            /chromosome="10"
            /map="10"
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        /clone_lib="RPCI-23 Female Mouse BAC"

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1..274998
/organism="Mus musculus"
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/clone="RP23-39C23"
/clone_lib="RPCI-23 Female Mouse BAC"

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ORIGIN

Query Match

85.0%; Score 17; DB 2: Length 274998;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTTAATGGAGTGGCT 20

Db 85254 GTTAATGGAGTGGCT 85270

RESULT 32

AC098451/c

LOCUS

DEFINITION

AC098451

AC098451.7

GI:22795073

HTG; HTGS PHASE1.

Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa;

Chordata; Craniata;

Vertebrata; Euteleostomi;

Mammalia; Eutheria;

Rodentia; Sciurognathi;

Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

Muzny,D.M., Adams,C.,

Adio-Oduola,B., Ali-

osman,F.R., Allen,C.,

Amara,L., Amaratunga,H.C.,

Are,J.R., Ayele,M., Banks,T.,

Barbata,J., Benton,J., Binage,K.,

Blankenburg,K., Bonnin,D.,

Bouck,J., Bowie,S., Brieva,M.,

Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C.,

Burrell,K.L., Byrd,N.C.,

Carroll,T.F., Carter,M., Cavazos,S.R.,

Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z.,

Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.C.,

Dathorne,S.R., David,R.,

Devalla,M.L., Davis,C., Davy-Carroll,L.,

Dederich,D.A.,

Delaney,K.R., Delgado,O.,

Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H.,

Dugan-Rocha,S., Durbin,K.J.,

Earnhart,C., Edgar,D.,

Edwards,C.C., Elhaj,C.,

Escotto,M.,

Falls,I., Ferraguto,D.,

Flegg,N., Ford,J.,

Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A.,

Garner,T., Garza,N.,

Gill,R.,

Gorell,J.H., Guevara,W.,

Gunaratne,P., Hale,S.,

Hamilton,K.,

Harris,C., Harris,K.,

Hart,M., Havlak,P.,

Hawes,A., Hernandez,J.,

Hernandez,O., Hodgson,A.,

Hogues,M., Holloway,C.,

Hollins,B.,

Homs,F., Howard,S.,

Huber,J., Hulyk,S.,

Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y.,

Johnson,R., Jolivet,S.,

Joudah,S.,

Karlsson,E., Kelly,S.,

Khan,U., King,L.,

Korvan,J., Kovar,C.,

Kratovic,J., Kurshil,A., Landry,N.,

Leal,B., Lewis,L.C., Lewis,L.,

Li,J., Li,Z., Lichtarge,O.,

Lieu,C., Liu,J., Liu,W.,

Louisseg,H.,

Lozano,R.J., Lu,X., Lucier,A.,

Lucier,R., Luna,R., Ma,J.,

Maheshwari,M., Mapa,P.,

Martin,R., Martindale,A.,

Martinez,E.,

Massey,E., Mayhew,E.,

McLeod,M.P., Meador,M.,

Mei,G., Metzker,M.,

Miner,G., Miner,Z.,

Mitchell,T., Mohabbat,K.,

Morgan,M., Morris,S.,

Moser,M., Neal,D.,

Newton,J., Newton,N.,

Nguyen,A., Nguyen,N.,

Nguyen,N.,

Nickerson,E., Nwokenko,S.,

Ogih,M., Okunou,G.,

Oragunye,N., Oviedo,R.,

Pace,A., Payton,B.,

Peery,J., Perez,L.,

Peters,L., Pickens,R.,

Primus,E., Pu,L.L.,

Quiles,M., Ren,Y.,

Rives,M., Rojas,A.,

Rojobokan,I., Rolfe,M.,

Ruiz,S., Savery,G.,

Scherer,S., Scott,G.,

Shen,H., Shoostari,N.,

Sisson,I.,

Sodergren,E., Sonaite,T.,

Sparks,A., Stanley,H.,

Stone,H.,

Sutton,A., Svatek,A.,

Tabor,P., Tamerisa,A.,

Tamaria,K., Tang,H.,

Tansey,J., Taylor,C.,

Taylor,T., Telford,B.,

Thomas,N., Thomas,S.,

Usmani,K., Vaquez,L.,

Vera,V., Villalob,D.,

Vinson,R., Wang,Q.,

Wang,S., Ward-Moore,S.,

Warren,R., Washington,C.,

Watlington,S.,

Williams,G., Williamson,A.,

Wleczyk,R., Wooden,S.,

Worley,K.,

Wu,C., Wu,Y., Wu,Y.F.,

Zhou,J., Zorrilla,S.,

Nelson,D.,

Weinstock,G., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 282383)

Worley,K.C.

Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 282383)

Worley,K.C.

Direct Submission

Unpublished

2 (bases 1 to 282383)

Worley,K.C.

Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

JOURNAL

COMMENT

Submitted (12-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 12, 2002 this sequence version replaced gi:21953456.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: T00A

Center clone name: CH230-2G23

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 161726 bases at least Q40

Consensus quality: 172494 bases at least Q30

Consensus quality: 179920 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 126 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

* 1471: contig of 1471 bp in length

* 1472: gap of unknown length

* 1572: contig of 1334 bp in length

* 2906: gap of unknown length

* 3005: contig of 1034 bp in length

* 4039: gap of unknown length

* 4040: contig of 1137 bp in length

* 4139: gap of unknown length

* 5277: gap of unknown length

* 5376: contig of 1020 bp in length

* 5377: gap of unknown length

* 6397: contig of 1055 bp in length

* 6497: gap of unknown length

* 7552: contig of 1274 bp in length

* 8926: gap of unknown length

* 9025: contig of 1056 bp in length

* 10081: contig of 1056 bp in length

* 10181: gap of unknown length

* 10182: contig of 1123 bp in length

* 11305: gap of unknown length

* 12883: contig of 1279 bp in length

* 12884: gap of unknown length

* 12783: contig of 1294 bp in length

* 14078: contig of 1187 bp in length

* 14177: gap of unknown length

* 15310: contig of 1133 bp in length

* 15410: gap of unknown length

* 15411: contig of 1065 bp in length

* 16475: gap of unknown length

* 16476: contig of 1371 bp in length

* 15756: gap of unknown length

* 17947: contig of 1187 bp in length

* 18047: gap of unknown length

* 19233: contig of 1008 bp in length

* 19334: contig of 1008 bp in length

* 20341: gap of unknown length

* 20441: contig of 1246 bp in length

* 21687: gap of unknown length

* 21688: contig of 1081 bp in length

* 21788: gap of unknown length

* 22868: contig of 1338 bp in length

* 22869: gap of unknown length

* 23969: contig of 1247 bp in length

* 24307: gap of unknown length

* 24406: contig of 1119 bp in length

* 25654: gap of unknown length

* 25753: contig of 1132 bp in length

* 25754: gap of unknown length

* 26972: contig of 1132 bp in length

* 26973: gap of unknown length

28105	28204:	gap of unknown length
28205	29264:	contig of 1060 bp in length
29265	29364:	gap of unknown length
29365	30377:	contig of 1013 bp in length
30378	30477:	gap of unknown length
30478	31521:	contig of 1044 bp in length
31522	31621:	gap of unknown length
31622	32663:	contig of 1042 bp in length
32664	32763:	gap of unknown length
32764	33799:	contig of 1036 bp in length
33800	33899:	gap of unknown length
33900	35111:	contig of 1212 bp in length
35112	35211:	gap of unknown length
35212	36284:	contig of 1073 bp in length
36285	36384:	gap of unknown length
36385	37694:	contig of 1310 bp in length
37695	37794:	gap of unknown length
37795	39489:	contig of 1695 bp in length
39490	39589:	gap of unknown length
39590	40899:	contig of 1310 bp in length
40900	40999:	gap of unknown length
41000	42616:	contig of 1617 bp in length
42617	44169:	contig of 1453 bp in length
44170	44269:	gap of unknown length
44270	45414:	contig of 1145 bp in length
45415	45514:	gap of unknown length
45515	47119:	contig of 1605 bp in length
47120	47219:	gap of unknown length
47220	48934:	contig of 1715 bp in length
48935	49034:	gap of unknown length
49035	50261:	contig of 1227 bp in length
50262	50361:	gap of unknown length
50362	51413:	contig of 1052 bp in length
51414	51513:	gap of unknown length
51514	52823:	contig of 1310 bp in length
52824	52923:	gap of unknown length
52924	54208:	contig of 1285 bp in length
54209	54308:	gap of unknown length
54309	55958:	contig of 1550 bp in length
55959	55959:	gap of unknown length
55960	57355:	contig of 1397 bp in length
57356	57455:	gap of unknown length
57456	58559:	contig of 1104 bp in length
58560	58659:	gap of unknown length
58660	59812:	contig of 1153 bp in length
59813	61196:	contig of 1284 bp in length
61197	62946:	gap of unknown length
62947	63046:	contig of 1650 bp in length
63047	64357:	contig of 1311 bp in length
64358	64457:	gap of unknown length
64458	65490:	contig of 1033 bp in length
65491	65590:	gap of unknown length
65591	67492:	contig of 1902 bp in length
67493	67592:	gap of unknown length
67593	69071:	contig of 1479 bp in length
69072	69171:	gap of unknown length
69172	71111:	contig of 1940 bp in length
71112	71211:	gap of unknown length
71212	72283:	contig of 1072 bp in length
72284	72383:	gap of unknown length
72384	73970:	contig of 1587 bp in length

Query Match 85.0%; Score 17; DB 2; Length 282383;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTTAAATGAGAGTGGCT 20
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 Db 205330 GTTAAATGAGAGTGGCT 205314
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RESULT 33
 AC106235/c
 LOCUS
 DEFINITION
 Rattus norvegicus clone CH230-79M6, *** SEQUENCING IN PROGRESS ***,
 7 unordered pieces.
 AC106235
 AC106235.4 GI:30579748
 HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
 Rattus norvegicus (Norway rat)
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

Muzny,D,Marie, Metzker,M, Lee, Abramson,S., Amin,A., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Ayodeji,M., Baca,E., Baden,H., Baylebechi,V., Blythe,J., Blythe,M., Barnstead,M., Benham,F., Biswal,D., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Kocha,S., Dunn,A., Durbin,K., Duval,B., Evans,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hires,S., Hladun,S.D., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacobs,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louisedge,H., Lozano,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K., Pastermak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shivartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Shedd,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villanana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
 Unpublished

2 (bases 1 to 346077)

Worley,K.C.

Direct Submission

Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 346077)

AUTHORS TITLE JOURNAL

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23321404.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKCG
Center clone name: CH230-79M6
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 276781 bases at least Q40
Consensus quality: 282820 bases at least Q30
Consensus quality: 286874 bases at least Q20
Estimated insert size: 300604; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1
* 13631: contig of 13631 bp in length
* 13632 13731: gap of unknown length
* 13732 30936: contig of 17205 bp in length
* 30937 31036: gap of unknown length
* 31037 44009: contig of 12973 bp in length
* 44010 44109: gap of unknown length
* 44110 339330: contig of 295221 bp in length
* 339331 339430: gap of unknown length
* 339431 341282: contig of 1862 bp in length
* 341293 341392: gap of unknown length
* 341393 342827: contig of 1435 bp in length
* 342828 342927: gap of unknown length
* 342928 346077: contig of 3150 bp in length.

FEATURES source

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/note="clone_boundary
clone_end:396
site:EcoRI
end sequence:BH320719"
13732..14767

misc_feature
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/note="wgs contig"
misc_feature
28817..30936
/note="wgs contig"
misc_feature
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/note="wgs contig"
misc_feature
40117..44009
/note="wgs contig"
misc_feature
44110..45164
/note="wgs contig"
misc_feature
55103..58734
/note="wgs contig"
misc_feature
94530..98001
/note="wgs contig"
misc_feature
100046..101790
/note="wgs contig"
misc_feature
complement(286270..287082)
/note="clone_boundary
clone_end:17
site:EcoRI
end sequence:BH320718"
332917..334384
/note="wgs end extension
clone_end:17"
misc_feature
337731..339330
/note="wgs end extension
clone_end:17"

ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 346077;
Best Local Similarity 100.0%; Pred.No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGTTAATCGAGAGTGGC 19

Db 254659 AGTTAATCGAGAGTGGC 254643

RESULT 34

Q0834336 2189 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 207 from Patent WO2004058805.
Q0834336
VERSION
Q0834336.1 GI:50833873
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS
Matsuda, A. and Yoneta, S.
TITLE
T cell activating gene
JOURNAL
Patent: WO 2004058805-A 207 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)

FEATURES

source
1. .2189
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
20..1936
/note="unnamed protein product"
/codon_start=1
/protein_id="CAH05383.1"
/db_xref="GI:50833874"

CDS

/translation="MOQYDLHLAQSMEGLNVAFAFMOLVKILLVDEERSVAHVTEA
DLFTHTLRLNNAHSGNAPEGLPQLMEVVRNRYEAMIDRAHGNGFMHSGISAS
BYDDPPGLREKAEYLLREWNLYHSAAGRDSTRKAFSGVQHQOGLIKDILITRF
FRLCMEVEISYRAQTEQHNPAANTMIKACYNLDAFVELIALLVKHSGEANT
VTKNLKNLGVVGLQHDVRSQFQQLPYHRI FIMLLLELNAPEHLETFNQ
TLTAFCTFHILRPTKAPGFVYAWLELISHRIFIARMLAHTPOQKGMVYQALLDIF
KYLAPFLRNVELTKPMQILYKGTUVRLLVLLHDPFPLCDYHYGFCVVPVPPNCIQURN
LILSAFPENNELPDFFTPNLKVDMLSEINIAPIRLITNFTGVMPPQPKDLDLSVLKTRS

PVTFLSDLSRNLQVNEPGRNVLQNLINALVLYVGTQAIHAIHNKSGTSPMSSTITHSA
HMDIFQNLAVDLDTGREGYFLFNAIANQLRYPNSHTYFSCITMLYFAEANTAEIOEQI
TRVLERLIVRPHFWGLLITFIETLKNPAKFWNEHVFCAPEIEKLFQSVQAQCMG
QKQAQQWMEGTGAS"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 2189;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
||||| ||||| ||||| |||||
DB 46 GCAGTCAATGGAGAGTGGCT 65

RESULT 35

CQ834338 2195 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 209 from Patent WO2004059805.
ACCESSION CQ834338
VERSION CQ834338.1 GI:50833875
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE

1 Matsuda, A. and Yoneta, S.
AUTHORS T cell activating gene
TITLE Patent: WO 2004058805-A 209 15-JUL-2004;
JOURNAL Asahi Kasei Pharma Corporation (JP)
FEATURES Location/Qualifiers
source 1..2195

source

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
20..1936
/note="unnamed protein product"

CDS

/codon_start=1
/protein_id="CAH05384.1"
/db_xref="GI:50833875"
/translation="MQQYDHLHAQSMENGLNVAFAFAMQLVKILLVDRSVAHVTEA
DLFTTIFLTKINAHSGNAPEGUPQLMEVVRNSYEAMIDRAHGPNFMHSGISQAS
EYDPPGLREKAEYLLREWNLYHSAAGRDSTKAFSAFYGMHQOQILKTDLLTRF
FRLCTMCVEISYRAQEQQHNPANPTIRAKCYHNLDAFVRLIALLVKHSGEATN
VTKINLKNLGIIVGVLLQDHDVROSEFQOLPYHRIIFMLLELNAPEHVLSTINQ
TLTAFCTHILRLTPKAPGVYAWLELISHRIFIARMLAHTPOQKGMWYAOILLDLF
KYLAFERNVELTKPMOILYKGLRVLVLLHDPPEFLCDHYHGFCDVIPPNCIQLRN
LILSAFERNRLPDPPTPNLKVDMLSINIAPIRLINFTGVMPQPKKOLDLSYKTRS
PVTLSDRNLQVNEPGRNVLQNLINALVLYVGTQAIHAIHNKSGTSPMSSTITHSA
HMDIFQNLAVDLDTGREGYFLFNAIANQLRYPNSHTYFSCITMLYFAEANTAEIOEQI
TRVLERLIVRPHFWGLLITFIETLKNPAKFWNEHVFCAPEIEKLFQSVQAQCMG
QKQAQQWMEGTGAS"

ORIGIN

Query Match 84.0%; Score 16.9; DB 6; Length 2195;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
||||| ||||| ||||| |||||
DB 46 GCAGTCAATGGAGAGTGGCT 65

RESULT 36

CQ783174 2637 bp DNA linear PAT 17-MAR-2004
LOCUS
DEFINITION Sequence 3314 from Patent EPI396543.
ACCESSION CQ783174
VERSION CQ783174.1 GI:45503105
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.

TITLE

JOURNAL

FEATURES

source

CDS

ORIGIN

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PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (19)... (2637).
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source
1..2637
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 84.0%; Score 16.8; DB 6; Length 2637;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||
Db 873 GCAGTCAATGGAGATGGCT 892
|||||

RESULT 38
AK075125 2637 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA FLJ90644 fis, clone PLACE1004168.
ACCESSION AK075125
VERSION AK075125.1 GI:22761010
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Ho, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahari, K., Masuno, Y., Ono, T., Okano, K., Ioshikawa, Y.,
Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
NEDO human cDNA sequencing project
Unpublished
REFERENCE
2 (bases 1 to 2637)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
Location/Qualifiers
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1004168"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="cloning vector: pME18SFL3"
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Query Match 84.0%; Score 16.8; DB 9; Length 2637;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATGGAGAGTGGCT 20
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Db 873 GCAGTCAATGGAGATGGCT 892
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RESULT 39
BD203717 2878 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in ovarian myoma tissue.
ACCESSION BD203717.1 GI:33013487
VERSION BD203717.1
KEYWORDS JP 2002511252-A/58.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2878)
Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and
Rosenthal, A.
Human nucleic acid sequence originating in ovarian myoma tissue
Patent: JP 2002511252-A 58 16-APR-2002;
METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002511252-A/58
PD 16-APR-2002
PF 07-APR-1999 JP 2000543588
PR 09-APR-1998 DE 198 17 557.4
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K38/00, A61K48/00, A61P15/00, A61P35/00, C07K14/82,
PC C07K16/32,
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/
PC 574,
PC C12N15/00, A61K37/02, C12N5/00
CC Human nucleic acid sequence originating in ovarian myoma CC
tissue
PH Key Location/Qualifiers
FT source 1..2878
/organism="Homo sapiens (human)"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 84.0%; Score 16.8; DB 6; Length 2878;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||
Db 193 GCAGTCAATGGAGATGGCT 212
|||||

RESULT 40
AX014872 2878 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 67 from Patent WO9953040.
ACCESSION AX014872
VERSION AX014872.1 GI:10041139
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and
Pilarsky, C.
Human nucleic acid sequences from ovarian tumour tissue
Patent: WO 9953040-A 67 21-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)

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        /organism="Homo sapiens"
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  Query Match
    Best Local Similarity 84.0%; Score 16.8; DB 6; Length 2878;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 1 GCAGTTAATGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
  Db 193 GCAGTCAATGAGAGTGGCT 212

  RESULT 41
  AF259793
  LOCUS
  DEFINITION
    Lycopersicon esculentum aldehyde oxidase (AO1) gene, partial cds.
  ACCESSION
    AF259793
  VERSION
    AF259793.1 GI:10764221
  KEYWORDS
    Lycopersicon esculentum (tomato)
  SOURCE
    Lycopersicon esculentum
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
  REFERENCE
    1 (bases 1 to 3560)
      Min, X., Okada, K., Brockmann, B., Koshiba, T. and Kamiya, Y.
      Molecular cloning and expression patterns of three putative
      functional aldehyde oxidase genes and isolation of two aldehyde
      oxidase pseudogenes in tomato
      Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
  AUTHORS
    Min, X., Okada, K., Brockmann, B., Koshiba, T. and Kamiya, Y.
  TITLE
    Direct Submission
  JOURNAL
    Submitted (21-APR-2000) Plant Function Laboratory, The Institute of
    Physical and Chemical Research (RIKEN), 2-1 Hiroseawa, Wako-Shi,
    Saitama 3510198, Japan
  FEATURES
    source
      Location/Qualifiers
        1. .3560
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          /mol_type="genomic DNA"
          /cultivar="Money-maker"
          /db_xref="taxon:4081"
          /tissue_type="leaf"
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          /gene="AO1"
          join(<1187. .1334,2676. .>3560)
          /gene="AO1"
          /product="aldehyde oxidase"
          join(1187. .1334,2676. .>3560)
          /gene="AO1"
          /EC number="1.2.3.1"
          /note="molybdenum cofactor-binding enzyme"
          /codon_start=1
          /product="aldehyde oxidase"
          /protein_id="AA022608.1"
          /db_xref="GI:10764222"
          /translation="MSERKQKGNLFAVNGERPELSPVSTTLHLFLRSETCYKSPK
          LGCEGCGACVVLISKYEPKPKVDFSSCLTLCSLNGCSITSLGNGTRDGP
          HSHTERFAGVACQCFPCLCWLSFSLVNTDKNKNPPGSKLTSBAENAI
          GNLCRTGYRPIDAKTFAADIDIELGNFWKKGDSKEMKVSRLPYETKPNST
          YPEFLKSNATNDSKIPWSPVSIKELNSLNFNTVNRGSKFLVWNGTGYKKE
          TQRYDHVDLRHPIELSIITKRQDTGIEVGATVTISFISVLKEESHNLGSGKLVSQ
          KLADHMEKIA"

  Query Match
    Best Local Similarity 84.0%; Score 16.8; DB 8; Length 3560;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 1 GCAGTTAATGAGAGTGGCT 20
      ||||| ||||| ||||| |||||
  Db 193 GCAGTCAATGAGAGTGGCT 212

  RESULT 42
  HSM01007
  LOCUS
  DEFINITION
    Homo sapiens mRNA; cDNA DKFp434N241 (from clone DKFp434N241);
    partial cds.
  ACCESSION
    AL117492
  VERSION
    AL117492.1 GI:5911979
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 3572)
      Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
      Direct Submission
      Submitted (15-SEP-1999) MIPS, Am Klopferspitz 18a, D-82152
      Martinsried, GERMANY
      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
      Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
      sequenced by DKFZ (German Cancer Research Center,
      Heidelberg/Germany) within the cDNA sequencing consortium of the
      German Genome Project.
      This clone (DKFp434N241) is available at the RZPD in Berlin.
      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
      Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
      information about the clone and the sequencing project is available
      at http://www.mips.biochem.mpg.de/proj/cDNA/.
  FEATURES
    source
      Location/Qualifiers
        1. .3572
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="DKFp434N241"
          /tissue_type="testis"
          /clone_lib="434 (synonym: htes3). Vector pSport1; host
          DH10B; sites NotI + SalI"
          /dev_stage="adult"
          1. .3572
          /gene="DKFp434N241"
          <1. .3303
          /note="KIAA1007, strong similarity to S.cerevisiae cdc39"
          /codon_start=1
          /product="hypothetical protein"
          /protein_id="CAB55960.1"
          /db_xref="GI:5911980"
          /db_xref="TrEMBL:Q9UFR8"
          /translation="LNLKFEIYLVCKNLADINELKPGNLLKDKRLKLNDELQLSAPK
          KDVKQPELPITTTTITTTTATVTPQPOQSYNDINVLVGLAGLPHITLNP
          TIFLQAHQKQCVQRAIERAVOELVHPVPSQISKIAMTTCEQIVRKQFALDSBSER
          MRIAHHMRLNLTAGMAMITREPLMSISTNLKNSFASALRTASPOQREMPOQAAQ
          LAQNCBLACCFIQKAVEKAGEMDKRLATEFELRKARQGRRYCDPVLVYQABR
          MPEQIRLKGVDPKQLAVFEFARNVPGFLPTNDLSOPTQFLAQPMQAWATDDVAQ
          IYDKITELQHLHAIPTLAMNPOAQLSLLEVVLVSRNSRDAALGLLQKAYEG
          LLDATSGADALLRYRECHLLVYLKALQDGRVAGSPKCNKQITCELEPDEYKNVE
          AVELLERNHLNMQVDLHLAQSNENGLNVAFAFMQLVILLVBSVAHVTEADL
          FHTIETLMRNHNSGNAPELPQLEMEVNSYNEAMIDRAHGPFNMFHSGISQABE
          DDPGLREKAYLLREWNLYHSAAGRSTKAFSAFVGQHQGLTKTDLLTRPFR
          LCTMCEVEISYRAQEQHNPAANTMIRAKCYHNLDAFVRLIALLVKSGETATVT
          KINLLNVLGVLLQDHDVRSQFPQYPIHRIIMLLLELNAEHWLETINFTLT
          TAFNCTHILRTPKAGFVVAWLELISHRFIARMLAHTPOQKGMWYQALLDLDFKY
          LAPFLRNVELTKPMQILYKGLTRVLLVLLHDFEFLCDYHGFCDVLPNCILORLNI
          LSAPPNNMLPDSPTENLKLMSLEINAPRIINTFTGNPPOFKDLSLYLKSPV
          TFLSDLSNLQVNSFNGRYNLQNALVLYGTQAIAHINKGTSPTMSYITHSAMH
          DIFONLAVLDLDTGRLFNALIANQLRYPNSTHYFECTVLYLFAFANETAIQEQITR
          VILLERLTVNRPHPWGLLITFIELIKNPAFKFWNHFVCAPIEKLFSQVAQCMGQK

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polya_site OAOQVMEGTGAS 3562 /gene="DFZp434N241"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 3572;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||

Db 1413 GCAGTCAATGGAGAGTGGCT 1432
|||||

RESULT 43
AF258808 4500 bp mRNA linear PLN 11-OCT-2000
LOCUS
DEFINITION Lycopersicon esculentum aldehyde oxidase (AO1) mRNA, complete cds.
ACCESSION AF258808
VERSION AF258808.1 GI:10764213
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 4500)
Min.X., Okada.K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Molecular cloning and expression patterns of three putative
functional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
20472051
PUBMED 11018259
REFERENCE 2 (bases 1 to 4500)
Min.X., Okada.K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Direct Submission
Submitted (20-APR-2000) Plant Function Laboratory, The Institute of
Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi,
Saitama 3510198, Japan
Location/Qualifiers
1. 4500
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Money-maker"
/db_xref="taxon:4081"
/chromosome="11"
/dev_stage="3 week-old wilting seedling"
1 4500
/gene="AO1"
181. 4286
/gene="AO1"
/EC_number="1.2.3.1"
/notes="molybdenum cofactor-binding enzyme"
/codon_start=1
/product="aldehyde oxidase"
/protein_id="AG22605.1"
/db_xref="GI:10764214"
/translation="MEERQKGNLVFVNGERFELPSVDPSTLLHLRSETCVKSPK
LGGEGGACVLLISKVEPKVEYDFSSCLTLCNLGCSITTSGLGNTRDGF
HSTHERFAYASQCQCTPGCLMSLFALVNTDKGNPPPGFKSLTSEAEANAIA
GNLCRTGYRIADACKYPAADIDIEDLGFNFSFKWKGDSKEMVSKLPPYDKNFTS
YPEFLKESATNLDSKYPWSPVSIKELWSLLFNVTNRGSKLVVNGTGTGYKE
TORDHYVDLRIH PELSIIRKPDQGTGIEVATVTSKFIISVLKESHNLGSKVLSQ
KLADHEKTAHSPFNASVGNLVMAQNGFPDSDIATLLGLSATVSLTSHGPNH
TWELLSPFLPSCKVLLSVCLPFKKDQSSHTSRFLFETRYRAAPRPHGNALAVNA
AFQADVHCNNGVLLNNIYAFAGYGTAKTRAKVVECLTGRMLSVHLYEALKLVK
LAVPBDGTLHPYRSLSAVSYFFFLPLTDVHPSISGGLLDINDISKEYSESN
NGCISGRKQKLLSSKQVPEYSPVSGEPLKIGIQAAMQAGEAVVDDIPSPNC
LHGAFIYTKPLAGVKGIOLEPNHLDITTIYKDIPTGGANTGAVTPPGSEPLFAD
LSRCAGDRTAFVADSORSADLAARTALIEYDITNVDSSAILTVEAEKSSFIQVPP
FOPEOIGDTKMAEADOKILSAELRFGSEYHMETOTALIPDENCMVVTSSOC
PENSQSMIASCLGVFAHNRVITRLGGAFGKFKVAMPVSTACALAAAYKLRPRVRY

gene

CDS

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 4500;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
|||||

Db 217 GCAGTTAATGGAGAGAGGT 236
|||||

RESULT 44
AF258812 4517 bp mRNA linear PLN 11-OCT-2000
LOCUS
DEFINITION Lycopersicon esculentum aldehyde oxidase (AO5) pseudogene, mRNA
sequence.
ACCESSION AF258812
VERSION AF258812.1 GI:10764220
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 4517)
Min.X., Okada.K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Molecular cloning and expression patterns of three putative
functional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
20472051
PUBMED 11018259
REFERENCE 2 (bases 1 to 4517)
Min.X., Okada.K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Direct Submission
Submitted (20-APR-2000) Plant Function Laboratory, The Institute of
Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi,
Saitama 3510198, Japan
Location/Qualifiers
1. 4517
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/db_xref="taxon:4081"
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1. 4517
/gene="AO5"
/note="aldehyde oxidase; putative; early termination of
translation"
/pseudo

gene

CDS

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 4517;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTTAATGGAGAGTGGCT 20
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Db 212 GCAGTTAATGGAGAGAGGT 231
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RESULT 45
AF258809 4631 bp mRNA linear PLN 11-OCT-2000
LOCUS

DEFINITION Lycopersicon esculentum aldehyde oxidase (AO2) mRNA, complete cds.
 ACCESSION AF258809
 VERSION AF258809.1 GI:10764215
 LOCUS
 DEFINITION Lycopersicon esculentum (tomato)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 4631)
 Min.X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
 Molecular cloning and expression patterns of three putative functional aldehyde oxidase genes and isolation of two aldehyde oxidase pseudogenes in tomato
 Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
 JOURNAL MEDLINE
 PUBMED
 20472051
 REFERENCE
 2 (bases 1 to 4631)
 Min.X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
 Direct Submission
 TITLE Submitted (20-APR-2000) Plant Function Laboratory, The Institute of Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi, Saitama 3510198, Japan
 JOURNAL
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 RYAGDRIAVVADQSADVAARTALVEYDTANVDSPLTVEAVEKSEFQIIPPLY
 PKQVDFSGMAEADHKLISAEVLGSEYVFMETOTALAI PEDNCMVVYSSQCP
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 KYDMGASFDVKLTNLTSTKSTMRSGEVOGSIYAEAIIEHVSSLLLEVDLVNKN
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 VPIVHEVSQSTFGKVIILQDGSIVVEVGIEIGQGLTKVQMTAYALGLIESWAE
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 SVDWPTLIROAQMSVHLAASVVPESSSKYNLFNGAAVSEVIEILTGETTILQSD
 IIVDCGSLNAPADLGOIEGAFVQGIQGFEMHEEYLNEDGLVSNSTWYKPTIDTI
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Query Match 84.0%; Score 16.8; DB 8; Length 4631;
 Best Local Similarity 90.0%; Pred. No. 5.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAGTTAATGGAGAGTGCT 20
 DB 399 GCAGTTAATGGAGAGTGCT 418

RESULT 46
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 LOCUS
 DEFINITION Sequence 229 from Patent WO0194629.
 ACCESSION AX329720
 VERSION AX329720.1 GI:18102698
 LOCUS
 DEFINITION Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Young,P.B., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrikan,S., Soppet,D.R. and Weaver,Z.
 Cancer gene determination and therapeutic screening using signature gene sets
 Patent: WO 0194629-A 229 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 JOURNAL
 FEATURES
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 1. .4977
 Location/Qualifiers
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 /db_xref="taxon:9606"
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RESULT 47
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 LOCUS
 DEFINITION Human mitogen induced nuclear orphan receptor (MINOR) mRNA,
 complete cds.
 ACCESSION U12767
 VERSION U12767.1 GI:924281
 LOCUS
 DEFINITION Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 4977)
 Hedvat,C.V. and Irving,S.G.
 The isolation and characterization of MINOR, a novel mitogen-inducible nuclear orphan receptor
 Mol. Endocrinol. 9 (12), 1692-1700 (1995)
 JOURNAL MEDLINE
 PUBMED
 96192925
 REFERENCE
 2 (bases 1 to 4977)
 Irving,S.G.
 Direct Submission
 TITLE Submitted (29-JUL-1994) Steven G. Irving, Department of Pathology, Georgetown University, School of Medicine, 3900 Reservoir Rd. NW, Washington, DC 20007, USA
 JOURNAL
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 1. .209
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ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 5122;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAGTAAATGGAGAGTGGCT 20

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Db 2973 GCAGTCATGGAGATGGCT 2992

RESULT 50

BC024317

LOCUS

BC024317 Homo sapiens KIAA1007 protein, mRNA (CDNA clone IMAGE:3913601),

partial cds.

BC024317

BC024317.1 GI:19354214

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5137)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunatratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Faney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,

Schnerich, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

PubMed

12477932

2 (bases 1 to 5137)

Strausberg, R.

Direct Submission

Submitted (01-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK
COMMENT

USA NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabp-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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Location/Qualifiers

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Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAGTTAATCGAGATGGCT 20
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Db 2973 GCAGTCAATCGAGATGGCT 2992

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 02:05:35 ; Search time 1761.58 Seconds
(without alignments)
62.385 Million cell updates/sec

Title: US-10-050-189A-7

Perfect score: 20

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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SUMMARIES

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4	15.8	79.0	182	9	US-09-796-692-299
5	15.8	79.0	182	9	US-09-796-692-453
6	15.8	79.0	182	9	US-09-796-692-3607
7	15.8	79.0	182	14	US-10-040-862-299
8	15.8	79.0	182	14	US-10-040-862-453
9	15.8	79.0	182	14	US-10-040-862-3607
10	15.8	79.0	182	16	US-10-057-475B-299
11	15.8	79.0	182	16	US-10-057-475B-453
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					Sequence 514, App
					Sequence 299, App
					Sequence 453, App
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C 86	15.2	76.0	2359	9	US-09-996-620-17	Sequence 17, Appl	C 159	14.8	74.0	2731748	17	US-10-297-7465A-1	Sequence 1, Appl
C 87	15.2	76.0	2869	16	US-10-041-018-103	Sequence 103, Appl	C 160	14.8	74.0	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
C 88	15.2	76.0	4447	18	US-10-425-115-111304	Sequence 111304, A	C 161	14.4	72.0	278	18	US-10-425-115-21678	Sequence 21678, A
C 89	15.2	76.0	16100	9	US-09-764-877-3698	Sequence 3698, Ap	C 162	14.4	72.0	307	16	US-10-242-535A-14457	Sequence 14457, A
C 90	15.2	76.0	16100	16	US-10-242-515-3698	Sequence 3698, Ap	C 163	14.4	72.0	307	16	US-10-085-783A-14457	Sequence 14457, A
C 91	15.2	76.0	18155	16	US-10-415-058-10	Sequence 10, Appl	C 164	14.4	72.0	331	16	US-10-276-774-626	Sequence 626, App
C 92	15.2	76.0	49600	16	US-10-459-262A-3	Sequence 3, Appl	C 165	14.4	72.0	337	18	US-10-425-115-65428	Sequence 65428, A
C 93	15.2	76.0	91552	16	US-10-415-058-5	Sequence 5, Appl	C 166	14.4	72.0	343	18	US-10-425-115-172196	Sequence 172196, A
C 94	15.2	76.0	93973	15	US-10-085-117-109	Sequence 109, Appl	C 167	14.4	72.0	360	18	US-10-425-115-49632	Sequence 49632, A
C 95	15.2	76.0	168575	15	US-10-478-194-1	Sequence 1, Appl	C 168	14.4	72.0	366	18	US-10-425-115-170848	Sequence 170848, A
C 96	15.2	76.0	374849	13	US-10-087-192-1627	Sequence 1627, Ap	C 169	14.4	72.0	403	18	US-10-425-115-67556	Sequence 67556, A
C 97	15.2	76.0	2731748	17	US-10-297-7465A-1	Sequence 1, Appl	C 170	14.4	72.0	413	18	US-09-18-995-17750	Sequence 17750, A
C 98	15	75.0	280	17	US-10-437-963-61873	Sequence 61873, A	C 171	14.4	72.0	422	18	US-10-425-115-101421	Sequence 101421, A
C 99	15	75.0	308	9	US-09-974-300-4461	Sequence 4461, Ap	C 172	14.4	72.0	463	18	US-10-425-115-167852	Sequence 167852, A
C 100	15	75.0	382	18	US-10-425-115-48807	Sequence 48807, A	C 173	14.4	72.0	468	16	US-10-242-535A-43713	Sequence 43713, A
C 101	15	75.0	533	13	US-10-027-632-198498	Sequence 198498, A	C 174	14.4	72.0	468	15	US-10-085-783A-43713	Sequence 43713, A
C 102	15	75.0	533	13	US-10-027-632-198499	Sequence 198499, A	C 175	14.4	72.0	505	17	US-10-437-963-44000	Sequence 44000, A
C 103	15	75.0	533	15	US-10-027-632-198498	Sequence 198498, A	C 176	14.4	72.0	514	17	US-10-437-963-74801	Sequence 74801, A
C 104	15	75.0	533	15	US-10-027-632-198499	Sequence 198499, A	C 177	14.4	72.0	524	18	US-10-363-345A-32877	Sequence 32877, A
C 105	15	75.0	537	15	US-10-106-698-2150	Sequence 2150, Ap	C 178	14.4	72.0	524	18	US-10-363-345A-32878	Sequence 32878, A
C 106	15	75.0	563	15	US-10-106-698-1423	Sequence 1423, Ap	C 179	14.4	72.0	706	15	US-10-012-697-40	Sequence 40, Appl
C 107	15	75.0	744	9	US-09-974-300-4531	Sequence 4531, Ap	C 180	14.4	72.0	715	15	US-10-424-599-94053	Sequence 94053, A
C 108	15	75.0	3840	17	US-10-437-963-12120	Sequence 12120, A	C 181	14.4	72.0	748	17	US-10-437-963-72972	Sequence 72972, A
C 109	15	75.0	298598	17	US-10-322-566-16	Sequence 16, Appl	C 182	14.4	72.0	751	13	US-10-027-632-110753	Sequence 110753, A
C 110	15	75.0	580073	15	US-10-205-220-1	Sequence 1, Appl	C 183	14.4	72.0	751	15	US-10-027-632-110753	Sequence 110753, A
C 111	14.8	74.0	240	16	US-10-242-535A-24203	Sequence 24203, A	C 184	14.4	72.0	779	17	US-10-437-963-52359	Sequence 52359, A
C 112	14.8	74.0	240	16	US-10-085-783A-24203	Sequence 24203, A	C 185	14.4	72.0	998	15	US-10-091-841-26	Sequence 26, Appl
C 113	14.8	74.0	380	16	US-10-425-115-183073	Sequence 183073, A	C 186	14.4	72.0	999	15	US-10-032-201B-9	Sequence 9, Appl
C 114	14.8	74.0	440	9	US-09-974-300-2539	Sequence 2539, Ap	C 187	14.4	72.0	999	15	US-10-032-201B-9	Sequence 40, Appl
C 115	14.8	74.0	463	18	US-10-674-124A-15346	Sequence 15346, A	C 188	14.4	72.0	1002	9	US-09-897-898-1	Sequence 1, Appl
C 116	14.8	74.0	495	16	US-10-621-501-2229	Sequence 2229, Ap	C 189	14.4	72.0	1002	9	US-09-897-898-2	Sequence 2, Appl
C 117	14.8	74.0	522	13	US-10-027-632-78717	Sequence 78717, A	C 190	14.4	72.0	1002	9	US-09-897-425-36	Sequence 36, Appl
C 118	14.8	74.0	522	15	US-10-027-632-78717	Sequence 78717, A	C 191	14.4	72.0	1002	9	US-09-897-425-37	Sequence 37, Appl
C 119	14.8	74.0	591	16	US-10-424-599-133577	Sequence 133577, A	C 192	14.4	72.0	1002	15	US-10-032-201B-8	Sequence 8, Appl
C 120	14.8	74.0	604	10	US-09-764-891-9085	Sequence 20960, A	C 193	14.4	72.0	1002	15	US-10-032-201B-10	Sequence 10, Appl
C 121	14.8	74.0	786	18	US-10-425-115-34326	Sequence 9085, Ap	C 194	14.4	72.0	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
C 122	14.8	74.0	882	16	US-10-282-122A-40512	Sequence 40512, A	C 195	14.4	72.0	1152	11	US-10-398-842A-2486	Sequence 2486, Ap
C 123	14.8	74.0	983	16	US-10-425-114-12031	Sequence 12031, A	C 196	14.4	72.0	1344	11	US-10-290-072-238	Sequence 238, App
C 124	14.8	74.0	1013	16	US-10-425-114-12031	Sequence 12031, A	C 197	14.4	72.0	1366	16	US-10-424-599-37944	Sequence 37944, A
C 125	14.8	74.0	1087	13	US-10-027-632-118486	Sequence 118486, A	C 198	14.4	72.0	1504	18	US-10-425-115-146408	Sequence 146408, A
C 126	14.8	74.0	1087	15	US-10-027-632-118486	Sequence 118486, A	C 199	14.4	72.0	1515	16	US-10-425-114-26169	Sequence 26169, A
C 127	14.8	74.0	1093	16	US-10-425-114-30448	Sequence 118486, A	C 200	14.4	72.0	1522	18	US-10-739-930-2865	Sequence 285, App
C 128	14.8	74.0	1093	16	US-10-425-114-30448	Sequence 118486, A	C 201	14.4	72.0	1523	16	US-10-425-114-20201	Sequence 20201, A
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C 130	14.8	74.0	1183	16	US-10-424-599-115765	Sequence 30478, A	C 203	14.4	72.0	1626	16	US-10-424-599-37943	Sequence 37943, A
C 131	14.8	74.0	1277	15	US-10-369-493-33917	Sequence 33917, A	C 204	14.4	72.0	1744	9	US-09-043-302-10	Sequence 10, Appl
C 132	14.8	74.0	1277	15	US-10-369-493-33917	Sequence 33917, A	C 205	14.4	72.0	2017	16	US-10-282-122A-33001	Sequence 33001, A
C 133	14.8	74.0	1500	16	US-10-425-114-36462	Sequence 335, App	C 206	14.4	72.0	2018	16	US-10-424-599-55709	Sequence 55709, A
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C 135	14.8	74.0	1594	18	US-10-425-115-131886	Sequence 131886, A	C 208	14.4	72.0	2307	15	US-10-120-988-314	Sequence 314, App
C 136	14.8	74.0	1621	15	US-10-369-493-42482	Sequence 42482, A	C 209	14.4	72.0	2344	18	US-10-425-115-163814	Sequence 163814, A
C 137	14.8	74.0	1676	16	US-10-425-114-16179	Sequence 18179, A	C 210	14.4	72.0	2399	17	US-10-437-963-71331	Sequence 71331, A
C 138	14.8	74.0	1685	16	US-10-425-114-29198	Sequence 29198, A	C 211	14.4	72.0	2943	15	US-10-369-493-46901	Sequence 46901, A
C 139	14.8	74.0	1781	14	US-10-198-846-10580	Sequence 10580, A	C 212	14.4	72.0	3093	18	US-10-417-375-92	Sequence 92, Appl
C 140	14.8	74.0	2073	17	US-10-437-963-52704	Sequence 52704, A	C 213	14.4	72.0	3094	15	US-10-028-384-9	Sequence 9, Appl
C 141	14.8	74.0	2205	18	US-10-425-115-183924	Sequence 183924, A	C 214	14.4	72.0	3287	9	US-09-043-302-1	Sequence 1, Appl
C 142	14.8	74.0	2464	18	US-10-425-115-173005	Sequence 173005, A	C 215	14.4	72.0	3787	9	US-09-897-898-13	Sequence 13, Appl
C 143	14.8	74.0	2575	16	US-10-425-115-163447	Sequence 163447, A	C 216	14.4	72.0	3787	9	US-09-897-425-48	Sequence 48, Appl
C 144	14.8	74.0	2585	9	US-09-867-701-10881	Sequence 10881, A	C 217	14.4	72.0	3787	15	US-10-032-201B-22	Sequence 22, Appl
C 145	14.8	74.0	2640	10	US-09-906-179A-218	Sequence 218, App	C 218	14.4	72.0	4545	9	US-09-897-898-18	Sequence 18, Appl
C 146	14.8	74.0	2655	16	US-10-108-260A-827	Sequence 827, App	C 219	14.4	72.0	4545	9	US-09-897-425-53	Sequence 53, Appl
C 147	14.8	74.0	2868	15	US-09-801-574-39	Sequence 39, Appl	C 220	14.4	72.0	4545	15	US-10-032-201B-27	Sequence 27, Appl
C 148	14.8	74.0	2958	15	US-10-369-493-41388	Sequence 41388, A	C 221	14.4	72.0	4546	15	US-09-897-898-15	Sequence 15, Appl
C 149	14.8	74.0	3063	17	US-10-437-963-16317	Sequence 16317, A	C 222	14.4	72.0	4546	9	US-09-897-425-50	Sequence 50, Appl
C 150	14.8	74.0	4845	16	US-10-607-095-15	Sequence 15, Appl	C 223	14.4	72.0	4546	15	US-10-032-201B-24	Sequence 24, Appl
C 151	14.8	74.0	4979	15	US-10-128-714-368	Sequence 368, App	C 224	14.4	72.0	4935	15	US-10-032-201B-33	Sequence 33, Appl
C 152	14.8	74.0	5055	15	US-10-128-714-368	Sequence 368, App	C 225	14.4	72.0	8841	9	US-09-954-531-1351	Sequence 1351, App
C 153	14.8	74.0	5214	18	US-10-425-115-167800	Sequence 167800, A	C 226	14.4	72.0	9043	15	US-10-116-275-304	Sequence 304, App
C 154	14.8	74.0	22055	11	US-09-997-722-145	Sequence 145, App	C 227	14.4	72.0	9953	9	US-09-764-847-1336	Sequence 1336, App
C 155	14.8	74.0	60815	13	US-10-087-192-52	Sequence 52, Appl	C 228	14.4	72.0	9953	14	US-10-092-154-1336	Sequence 1336, App
C 156	14.8	74.0	76201	16	US-10-439-703-84	Sequence 84, Appl	C 229	14.4	72.0	10236	14	US-10-114-170-240	Sequence 240, App
C 157	14.8	74.0	493631	13	US-10-087-192-205	Sequence 205, App	C 230	14.4	72.0	11189	9	US-09-764-847-1335	Sequence 1335, App
C 158	14.8	74.0	684707	16	US-10-398-221-9	Sequence 9, Appl	C 231	14.4	72.0	11189	14	US-10-092-154-1335	Sequence 1335, App

232	14.4	72.0	12003	17	US-10-775-169-331	Sequence 331, App	305	14.2	71.0	501	15	US-10-027-632-74739	Sequence 74739, A
C 233	14.4	72.0	12860	9	US-09-070-927A-144	Sequence 144, App	306	14.2	71.0	522	17	US-10-437-963-190187	Sequence 190187, A
234	14.4	72.0	15686	16	US-10-415-058-3	Sequence 3, Appl	C 307	14.2	71.0	534	13	US-10-027-632-194047	Sequence 194047, A
C 235	14.4	72.0	54810	18	US-10-417-375-91	Sequence 91, Appl	C 308	14.2	71.0	534	15	US-10-027-632-194047	Sequence 194047, A
C 236	14.4	72.0	92647	13	US-10-087-192-1267	Sequence 1267, Ap	C 309	14.2	71.0	534	17	US-10-767-701-9406	Sequence 9406, Ap
C 237	14.4	72.0	116422	13	US-10-087-192-1195	Sequence 1195, Ap	C 310	14.2	71.0	534	17	US-10-767-701-1215	Sequence 1215, Ap
C 238	14.4	72.0	155579	15	US-10-085-117-283	Sequence 283, App	C 311	14.2	71.0	559	9	US-09-834-975-331	Sequence 331, App
C 239	14.4	72.0	252907	18	US-10-417-375-66	Sequence 66, Appl	C 312	14.2	71.0	559	9	US-10-767-701-24202	Sequence 24202, A
C 240	14.4	72.0	744802	15	US-10-292-798-1369	Sequence 1369, Ap	C 313	14.2	71.0	566	9	US-09-834-975-331	Sequence 331, App
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C 242	14.4	72.0	1830121	16	US-10-329-670-1	Sequence 1, Appl	C 315	14.2	71.0	567	13	US-10-027-632-51215	Sequence 51215, A
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C 244	14.4	72.0	2256646	17	US-10-470-565-1	Sequence 1, Appl	C 317	14.2	71.0	571	16	US-10-154-884B-8380	Sequence 8380, Ap
C 245	14.2	71.0	231	15	US-10-357-028-32	Sequence 32, Appl	C 318	14.2	71.0	571	16	US-10-764-324-8380	Sequence 8380, Ap
C 246	14.2	71.0	238	18	US-10-425-115-130711	Sequence 130711, A	C 319	14.2	71.0	571	17	US-10-425-115-130711	Sequence 130711, A
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C 248	14.2	71.0	281	15	US-10-357-028-19	Sequence 19, Appl	C 321	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 249	14.2	71.0	285	18	US-10-425-115-11848	Sequence 11848, A	C 322	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
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C 254	14.2	71.0	279	9	US-09-796-692-446	Sequence 446, App	C 327	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 255	14.2	71.0	279	9	US-09-796-692-3457	Sequence 3457, App	C 328	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 256	14.2	71.0	279	14	US-10-040-862-289	Sequence 289, App	C 329	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
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C 262	14.2	71.0	279	16	US-10-154-884B-446	Sequence 446, App	C 335	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 263	14.2	71.0	279	16	US-10-154-884B-446	Sequence 446, App	C 336	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
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C 265	14.2	71.0	279	17	US-10-764-324-289	Sequence 289, App	C 338	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
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C 267	14.2	71.0	279	17	US-10-764-324-3457	Sequence 3457, App	C 340	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 268	14.2	71.0	289	16	US-10-424-599-86178	Sequence 86178, A	C 341	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 269	14.2	71.0	289	16	US-10-424-599-86178	Sequence 86178, A	C 342	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 270	14.2	71.0	301	9	US-09-974-300-3460	Sequence 3460, App	C 343	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 271	14.2	71.0	309	16	US-10-424-599-89506	Sequence 89506, A	C 344	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 272	14.2	71.0	310	16	US-10-242-535A-17983	Sequence 17983, A	C 345	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 273	14.2	71.0	310	16	US-10-085-783A-17983	Sequence 17983, A	C 346	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 274	14.2	71.0	310	18	US-10-425-115-134558	Sequence 134558, A	C 347	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 275	14.2	71.0	322	9	US-09-960-352-6767	Sequence 6767, App	C 348	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 276	14.2	71.0	357	17	US-10-437-963-71768	Sequence 71768, A	C 349	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 277	14.2	71.0	360	9	US-09-778-320-60	Sequence 60, Appl	C 350	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 278	14.2	71.0	360	9	US-09-910-689-60	Sequence 60, Appl	C 351	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 279	14.2	71.0	360	13	US-10-010-742-60	Sequence 60, Appl	C 352	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 280	14.2	71.0	360	17	US-10-714-389-60	Sequence 60, Appl	C 353	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 281	14.2	71.0	366	17	US-10-717-296-60	Sequence 60, Appl	C 354	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 282	14.2	71.0	366	18	US-10-425-115-118495	Sequence 118495, A	C 355	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 283	14.2	71.0	382	18	US-10-674-124A-28259	Sequence 28259, A	C 356	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 284	14.2	71.0	383	13	US-10-079-623-201	Sequence 201, App	C 357	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 285	14.2	71.0	383	18	US-10-425-115-166694	Sequence 166694, A	C 358	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 286	14.2	71.0	394	18	US-10-425-115-165208	Sequence 165208, A	C 359	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 287	14.2	71.0	415	16	US-09-918-995-16895	Sequence 16895, A	C 360	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 288	14.2	71.0	421	16	US-10-242-535A-7075	Sequence 7075, App	C 361	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 289	14.2	71.0	421	16	US-10-065-783A-7075	Sequence 7075, App	C 362	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 290	14.2	71.0	459	13	US-10-027-632-85449	Sequence 85449, A	C 363	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 291	14.2	71.0	459	15	US-10-027-632-85449	Sequence 85449, A	C 364	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 292	14.2	71.0	459	16	US-10-424-599-75284	Sequence 75284, A	C 365	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 293	14.2	71.0	460	9	US-09-974-300-4906	Sequence 4906, App	C 366	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 294	14.2	71.0	470	9	US-09-962-436-347	Sequence 347, App	C 367	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 295	14.2	71.0	474	16	US-10-282-122A-20687	Sequence 20687, A	C 368	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 296	14.2	71.0	479	9	US-09-864-761-2330	Sequence 2330, App	C 369	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 297	14.2	71.0	479	9	US-09-796-692-7879	Sequence 7879, App	C 370	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 298	14.2	71.0	479	14	US-10-040-862-7879	Sequence 7879, App	C 371	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 299	14.2	71.0	479	16	US-10-057-475B-7879	Sequence 7879, App	C 372	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 300	14.2	71.0	479	16	US-10-154-884B-7879	Sequence 7879, App	C 373	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 301	14.2	71.0	479	17	US-10-764-324-7879	Sequence 324-7879	C 374	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 302	14.2	71.0	496	17	US-10-767-701-3473	Sequence 3473, App	C 375	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 303	14.2	71.0	500	13	US-10-027-632-75547	Sequence 75547, A	C 376	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A
C 304	14.2	71.0	501	13	US-10-027-632-74739	Sequence 74739, A	C 377	14.2	71.0	580	18	US-10-425-115-130711	Sequence 130711, A

C 378	14.2	71.0	963	16	US-10-282-122A-27676	Sequence 27676, A	C 451	14.2	71.0	159400	17	US-10-450-826-33	Sequence 33, Appl
C 379	14.2	71.0	994	10	US-09-814-353-20556	Sequence 20556, A	452	14.2	71.0	225734	17	US-10-322-696-13	Sequence 13, Appl
C 380	14.2	71.0	1051	16	US-10-425-114-12939	Sequence 12939, A	453	14.2	71.0	296405	13	US-10-087-192-1036	Sequence 1036, Ap
C 381	14.2	71.0	1074	13	US-10-027-632-118361	Sequence 118361, A	454	14.2	71.0	358246	15	US-10-292-798-1095	Sequence 1095, Ap
C 382	14.2	71.0	1074	15	US-10-027-632-118361	Sequence 118361, A	455	14.2	71.0	358246	15	US-10-292-798-1095	Sequence 1095, Ap
C 383	14.2	71.0	1125	9	US-09-834-975-995	Sequence 995, App	C 456	14.2	71.0	400660	17	US-10-388-838-68	Sequence 68, Appl
C 384	14.2	71.0	1152	17	US-10-437-963-84143	Sequence 84143, A	C 457	14.2	71.0	518360	17	US-10-367-094-125	Sequence 125, App
C 385	14.2	71.0	1172	16	US-10-425-114-13073	Sequence 13073, A	C 458	14.2	71.0	561515	17	US-10-741-601-5682	Sequence 5682, Ap
C 386	14.2	71.0	1177	9	US-09-778-844-87	Sequence 87, Appl	C 459	14.2	71.0	786431	15	US-10-412-277-3	Sequence 3, Appl1
C 387	14.2	71.0	1182	17	US-10-437-963-54956	Sequence 54956, A	C 460	14.2	71.0	786431	15	US-10-425-115-166224	Sequence 166224, A
C 388	14.2	71.0	1268	17	US-10-437-963-6413	Sequence 6413, Ap	C 461	14.2	71.0	336	18	US-10-425-115-166224	Sequence 166224, A
C 389	14.2	71.0	1295	17	US-10-767-701-14452	Sequence 14452, A	C 462	14.2	71.0	357	16	US-10-424-599-130919	Sequence 130919, A
C 390	14.2	71.0	1413	17	US-10-767-701-12038	Sequence 12038, A	C 463	14.2	71.0	4053	16	US-10-424-599-82571	Sequence 82571, A
C 391	14.2	71.0	1485	17	US-10-437-963-69410	Sequence 69410, A	C 464	14.2	71.0	472	16	US-10-424-599-17637	Sequence 17637, A
C 392	14.2	71.0	1616	17	US-10-437-963-78180	Sequence 78180, A	C 465	14.2	71.0	479	9	US-09-864-761-2243	Sequence 2243, Ap
C 393	14.2	71.0	1634	9	US-09-938-842A-3400	Sequence 3400, Ap	C 466	14.2	71.0	516	10	US-09-918-995-4483	Sequence 4483, Ap
C 394	14.2	71.0	1634	11	US-09-938-842A-3400	Sequence 3400, Ap	C 467	14.2	71.0	587	13	US-10-027-632-39553	Sequence 39553, A
C 395	14.2	71.0	1646	17	US-10-767-701-14617	Sequence 14617, A	C 468	14.2	71.0	587	13	US-10-027-632-314335	Sequence 314335, A
C 396	14.2	71.0	1686	17	US-10-437-963-43536	Sequence 43536, A	C 469	14.2	71.0	587	13	US-10-027-632-314336	Sequence 314336, A
C 397	14.2	71.0	1733	16	US-10-425-114-23293	Sequence 23293, A	C 470	14.2	71.0	587	15	US-10-027-632-39553	Sequence 39553, A
C 398	14.2	71.0	1733	18	US-10-425-114-23293	Sequence 23293, A	C 471	14.2	71.0	587	15	US-10-027-632-314335	Sequence 314335, A
C 399	14.2	71.0	1914	17	US-10-437-963-25753	Sequence 25753, A	C 472	14.2	71.0	593	13	US-10-027-632-314336	Sequence 314336, A
C 400	14.2	71.0	1996	16	US-10-424-599-123162	Sequence 123162, A	C 473	14.2	71.0	593	13	US-10-027-632-241354	Sequence 241354, A
C 401	14.2	71.0	2012	18	US-10-425-115-84505	Sequence 84505, A	C 474	14.2	71.0	687	13	US-10-027-632-241354	Sequence 241354, A
C 402	14.2	71.0	2048	9	US-09-822-849A-232	Sequence 232, App	C 475	14.2	71.0	1132	10	US-10-040-739-989	Sequence 989, App
C 403	14.2	71.0	2079	17	US-10-437-963-59334	Sequence 59334, A	C 476	14.2	71.0	1769	18	US-10-425-115-86768	Sequence 86768, A
C 404	14.2	71.0	2137	16	US-10-282-122A-21557	Sequence 21557, A	C 477	14.2	71.0	2596	13	US-10-027-632-265115	Sequence 265115, A
C 405	14.2	71.0	2157	16	US-10-398-221-3547	Sequence 3547, Ap	C 478	14.2	71.0	2596	13	US-10-027-632-265115	Sequence 265115, A
C 406	14.2	71.0	2183	16	US-10-425-114-32370	Sequence 32370, A	C 479	14.2	71.0	3493	16	US-10-424-599-115517	Sequence 115517, A
C 407	14.2	71.0	2192	18	US-10-425-115-125877	Sequence 125877, A	C 480	14.2	71.0	3669	17	US-10-697-828-22	Sequence 22, Appl
C 408	14.2	71.0	2217	17	US-10-322-696-104	Sequence 104, App	C 481	14.2	71.0	3733	17	US-10-697-828-18	Sequence 18, Appl
C 409	14.2	71.0	2266	15	US-10-205-219-18	Sequence 18, Appl	C 482	14.2	71.0	4133	18	US-10-475-446-34	Sequence 34, Appl
C 410	14.2	71.0	2336	16	US-10-424-599-137007	Sequence 137007, A	C 483	14.2	71.0	4599	17	US-10-697-828-14	Sequence 14, Appl
C 411	14.2	71.0	2359	16	US-10-108-260A-83	Sequence 83, Appl	C 484	14.2	71.0	5145	10	US-09-814-353-19610	Sequence 19610, A
C 412	14.2	71.0	2937	9	US-09-974-300-2288	Sequence 2288, Ap	C 485	14.2	71.0	5145	15	US-10-172-118-1499	Sequence 1499, Ap
C 413	14.2	71.0	3135	16	US-10-108-260A-617	Sequence 617, App	C 486	14.2	71.0	5145	16	US-10-342-887-1499	Sequence 1499, Ap
C 414	14.2	71.0	3279	9	US-09-432-126-11	Sequence 11, Appl	C 487	14.2	71.0	5559	9	US-09-783-066-6	Sequence 6, Appl1
C 415	14.2	71.0	3518	15	US-10-369-493-26239	Sequence 26239, A	C 488	14.2	71.0	27150	17	US-10-697-828-20	Sequence 20, Appl
C 416	14.2	71.0	3907	9	US-09-707-927A-343	Sequence 343, App	C 489	14.2	71.0	69081	13	US-10-087-192-1132	Sequence 1192, Ap
C 417	14.2	71.0	4235	16	US-10-476-774-724	Sequence 724, App	C 490	14.2	71.0	119211	16	US-10-672-787-40	Sequence 40, Appl
C 418	14.2	71.0	4235	16	US-10-296-115-496	Sequence 496, App	C 491	14.2	71.0	213040	13	US-10-087-192-856	Sequence 856, App
C 419	14.2	71.0	4425	17	US-10-706-424-9	Sequence 9, Appl1	C 492	14.2	71.0	275449	13	US-10-087-192-520	Sequence 520, App
C 420	14.2	71.0	4425	18	US-10-609-113-43	Sequence 43, Appl	C 493	14.2	71.0	317876	17	US-10-741-601-5629	Sequence 5629, App
C 421	14.2	71.0	4425	18	US-10-754-115-44	Sequence 44, Appl	C 494	14.2	71.0	330973	13	US-10-087-192-1498	Sequence 1498, App
C 422	14.2	71.0	4592	14	US-10-193-692-1	Sequence 1, Appl1	C 495	14.2	71.0	438892	13	US-10-087-192-454	Sequence 454, App
C 423	14.2	71.0	5768	10	US-09-873-367C-134	Sequence 134, App	C 496	14.2	71.0	2140405	13	US-10-027-632-76212	Sequence 76212, A
C 424	14.2	71.0	8937	17	US-10-437-963-18559	Sequence 18559, A	C 497	14.2	71.0	2140405	15	US-10-027-632-76212	Sequence 76212, A
C 425	14.2	71.0	9377	13	US-10-194-163-1002	Sequence 1002, Ap	C 498	13.8	69.0	177	17	US-10-437-963-69455	Sequence 69455, A
C 426	14.2	71.0	11367	17	US-10-471-450-42	Sequence 42, Appl	C 499	13.8	69.0	247	9	US-09-193-881-9	Sequence 9, Appl1
C 427	14.2	71.0	17761	9	US-09-764-847-1596	Sequence 1596, Ap	C 500	13.8	69.0	247	15	US-10-338-395-9	Sequence 9, Appl1
C 428	14.2	71.0	17761	14	US-10-092-154-1596	Sequence 1596, Ap	C 501	13.8	69.0	265	18	US-10-425-115-128454	Sequence 128454, A
C 429	14.2	71.0	25891	13	US-10-087-192-1657	Sequence 1657, Ap	C 502	13.8	69.0	272	15	US-10-102-524-196	Sequence 196, App
C 430	14.2	71.0	26385	17	US-10-322-696-103	Sequence 103, App	C 503	13.8	69.0	274	10	US-09-535-459-739	Sequence 739, App
C 431	14.2	71.0	27062	10	US-09-764-891-8034	Sequence 8034, Ap	C 504	13.8	69.0	281	16	US-10-242-535A-8100	Sequence 8100, Ap
C 432	14.2	71.0	29934	13	US-10-087-193-1837	Sequence 1837, Ap	C 505	13.8	69.0	281	16	US-10-085-783A-8100	Sequence 8100, Ap
C 433	14.2	71.0	30013	9	US-09-764-877-3297	Sequence 3297, Ap	C 506	13.8	69.0	290	17	US-10-437-963-92170	Sequence 92170, A
C 434	14.2	71.0	30013	16	US-10-242-513-3297	Sequence 3297, Ap	C 507	13.8	69.0	315	16	US-10-424-599-32277	Sequence 32277, A
C 435	14.2	71.0	32585	13	US-10-087-192-7	Sequence 7, Appl1	C 508	13.8	69.0	327	16	US-10-424-599-94699	Sequence 94699, A
C 436	14.2	71.0	33352	11	US-09-997-722-112	Sequence 112, App	C 509	13.8	69.0	331	18	US-10-425-115-90997	Sequence 90997, A
C 437	14.2	71.0	33963	15	US-10-292-798-617	Sequence 617, App	C 510	13.8	69.0	333	16	US-10-282-122A-28848	Sequence 28848, A
C 438	14.2	71.0	39292	15	US-10-004-113-52	Sequence 52, Appl	C 511	13.8	69.0	336	16	US-10-282-122A-28790	Sequence 28790, A
C 439	14.2	71.0	44325	11	US-09-997-722-226	Sequence 226, App	C 512	13.8	69.0	337	17	US-10-855-595-1	Sequence 1, Appl1
C 440	14.2	71.0	53328	17	US-10-741-601-5639	Sequence 5639, Ap	C 513	13.8	69.0	354	17	US-10-437-963-15946	Sequence 15946, A
C 441	14.2	71.0	59817	16	US-10-052-482-190	Sequence 190, App	C 514	13.8	69.0	357	18	US-10-425-115-30296	Sequence 30296, A
C 442	14.2	71.0	70215	13	US-10-087-192-217	Sequence 217, App	C 515	13.8	69.0	368	18	US-10-425-115-100623	Sequence 100623, A
C 443	14.2	71.0	73507	13	US-10-087-192-147	Sequence 147, App	C 516	13.8	69.0	375	18	US-10-674-124A-7143	Sequence 7143, Ap
C 444	14.2	71.0	79799	13	US-10-087-192-346	Sequence 346, App	C 517	13.8	69.0	383	18	US-10-674-124A-19928	Sequence 19928, A
C 445	14.2	71.0	81826	14	US-10-175-523-137	Sequence 137, App	C 518	13.8	69.0	385	18	US-10-425-115-126618	Sequence 126618, A
C 446	14.2	71.0	93538	17	US-09-997-722-154	Sequence 154, App	C 519	13.8	69.0	387	13	US-09-878-178-1341	Sequence 1341, Ap
C 447	14.2	71.0	96594	11	US-09-997-722-43	Sequence 43, Appl	C 520	13.8	69.0	387	14	US-10-046-935-1341	Sequence 1341, Ap
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C 449	14.2	71.0	105550	17	US-10-367-094-90	Sequence 90, App	C 522	13.8	69.0	388	9	US-09-860-107-1561	Sequence 1561, App
C 450	14.2	71.0	139613	17	US-10-367-094-90	Sequence 90, App	C 523	13.8	69.0	388	10	US-09-873-367C-649	Sequence 649, App

C 524	13.8	69.0	400	9	US-09-783-590-738	Sequence 738, App	597	13.8	69.0	759	15	US-10-027-632-160988	Sequence 160988,
525	13.8	69.0	403	18	US-10-425-115-102855	Sequence 102855, App	C 598	13.8	69.0	760	15	US-10-172-118-1661	Sequence 1661, App
526	13.8	69.0	405	16	US-10-282-122A-18655	Sequence 18655, A	C 599	13.8	69.0	760	16	US-10-342-887-1661	Sequence 1661, App
527	13.8	69.0	405	18	US-10-653-047-1398	Sequence 1398, App	C 600	13.8	69.0	760	17	US-10-755-889-497	Sequence 497, App
528	13.8	69.0	419	18	US-10-425-115-130819	Sequence 130819, App	C 601	13.8	69.0	764	9	US-09-974-298-187	Sequence 187, App
C 529	13.8	69.0	424	9	US-09-998-598-882	Sequence 882, App	C 602	13.8	69.0	798	9	US-09-974-298-185	Sequence 185, App
C 530	13.8	69.0	425	10	US-09-918-995-36642	Sequence 36642, App	C 603	13.8	69.0	803	9	US-09-822-830A-537	Sequence 537, App
C 531	13.8	69.0	427	16	US-10-424-599-45665	Sequence 45665, A	C 604	13.8	69.0	813	16	US-10-282-122A-27933	Sequence 27933, A
C 532	13.8	69.0	432	11	US-09-733-637A-4331	Sequence 4331, App	C 605	13.8	69.0	822	16	US-10-282-122A-27933	Sequence 27933, A
C 533	13.8	69.0	441	18	US-10-674-124A-22191	Sequence 22191, A	C 606	13.8	69.0	884	9	US-09-819-144A-3	Sequence 3, Appli
534	13.8	69.0	450	16	US-10-424-599-52713	Sequence 52713, A	C 607	13.8	69.0	889	15	US-10-369-493-27136	Sequence 27136, A
535	13.8	69.0	453	16	US-10-424-599-107346	Sequence 107346, A	C 608	13.8	69.0	891	9	US-09-925-299-128	Sequence 128, App
C 536	13.8	69.0	460	13	US-09-960-352-9088	Sequence 9088, App	C 609	13.8	69.0	891	10	US-09-925-299-128	Sequence 128, App
C 537	13.8	69.0	501	9	US-10-027-632-266568	Sequence 266568, App	C 610	13.8	69.0	891	13	US-10-027-632-262721	Sequence 262721, App
C 538	13.8	69.0	501	15	US-10-027-632-266568	Sequence 266568, App	C 611	13.8	69.0	913	13	US-10-027-632-262721	Sequence 262721, App
C 539	13.8	69.0	506	9	US-09-878-178-1973	Sequence 1973, App	C 612	13.8	69.0	913	15	US-10-027-632-262722	Sequence 262722, App
C 540	13.8	69.0	506	13	US-10-046-935-1973	Sequence 1973, App	C 613	13.8	69.0	913	15	US-10-027-632-262722	Sequence 262722, App
C 541	13.8	69.0	506	14	US-10-146-502-1973	Sequence 1973, App	C 614	13.8	69.0	918	9	US-09-974-300-4593	Sequence 4593, App
C 542	13.8	69.0	520	17	US-10-437-963-78847	Sequence 78847, A	C 615	13.8	69.0	924	17	US-10-343-561-7	Sequence 7, Appli
543	13.8	69.0	537	13	US-10-027-632-211175	Sequence 211175, App	C 616	13.8	69.0	949	16	US-10-425-114-10386	Sequence 10386, A
544	13.8	69.0	537	15	US-10-027-632-211175	Sequence 211175, App	C 617	13.8	69.0	972	16	US-10-425-114-6605	Sequence 6605, App
C 545	13.8	69.0	537	17	US-10-343-561-26	Sequence 26, Appli	C 618	13.8	69.0	972	16	US-10-424-599-40443	Sequence 40443, A
C 546	13.8	69.0	548	17	US-10-767-701-31294	Sequence 31294, A	C 619	13.8	69.0	1000	17	US-10-424-599-40443	Sequence 8, Appli
547	13.8	69.0	549	16	US-10-398-221-402	Sequence 814, App	C 620	13.8	69.0	1000	17	US-10-343-561-25	Sequence 25, Appli
548	13.8	69.0	551	9	US-09-879-536-814	Sequence 814, App	C 621	13.8	69.0	1000	17	US-10-343-561-30	Sequence 30, Appli
549	13.8	69.0	558	16	US-10-275-026A-149	Sequence 149, App	C 622	13.8	69.0	1112	18	US-10-739-930-4759	Sequence 4759, App
550	13.8	69.0	579	13	US-10-027-632-61822	Sequence 61822, A	C 623	13.8	69.0	1112	16	US-10-282-122A-29528	Sequence 29528, A
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552	13.8	69.0	579	15	US-10-027-632-61822	Sequence 61822, A	C 625	13.8	69.0	1127	16	US-10-282-122A-12100	Sequence 12100, A
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C 554	13.8	69.0	583	13	US-10-027-632-262974	Sequence 262974, A	C 627	13.8	69.0	1172	15	US-10-205-194-38	Sequence 38, Appli
C 555	13.8	69.0	583	17	US-10-027-632-262974	Sequence 262974, A	C 628	13.8	69.0	1191	16	US-10-424-599-29003	Sequence 29003, A
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557	13.8	69.0	598	13	US-10-027-632-240602	Sequence 240602, A	C 630	13.8	69.0	1209	16	US-10-282-122A-10008	Sequence 10008, A
558	13.8	69.0	598	13	US-10-027-632-240602	Sequence 240602, A	C 631	13.8	69.0	1218	16	US-10-282-122A-10008	Sequence 10008, A
559	13.8	69.0	598	15	US-10-027-632-240604	Sequence 240604, A	C 632	13.8	69.0	1230	16	US-10-282-122A-30946	Sequence 30946, A
560	13.8	69.0	598	15	US-10-027-632-240602	Sequence 240602, A	C 633	13.8	69.0	1264	17	US-10-767-701-11346	Sequence 11346, A
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C 562	13.8	69.0	602	15	US-10-027-632-240604	Sequence 240604, A	C 635	13.8	69.0	1341	17	US-10-437-963-48395	Sequence 48395, A
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C 564	13.8	69.0	602	15	US-10-062-599-40	Sequence 40, Appli	C 637	13.8	69.0	1347	15	US-10-345-820-82	Sequence 82, Appli
C 565	13.8	69.0	607	9	US-09-910-430-2	Sequence 2, Appli	C 638	13.8	69.0	1377	15	US-10-424-599-80362	Sequence 80362, A
C 566	13.8	69.0	607	14	US-10-165-603A-2	Sequence 2, Appli	C 639	13.8	69.0	1392	15	US-10-320-800-29	Sequence 29, Appli
C 567	13.8	69.0	614	17	US-10-767-701-23603	Sequence 23603, A	C 640	13.8	69.0	1428	16	US-10-282-122A-27304	Sequence 27304, A
C 568	13.8	69.0	627	18	US-10-425-115-176515	Sequence 176515, A	C 641	13.8	69.0	1462	16	US-10-425-114-15534	Sequence 15534, A
569	13.8	69.0	645	18	US-10-425-115-120151	Sequence 120151, A	C 642	13.8	69.0	1575	16	US-10-424-599-32127	Sequence 32127, A
C 570	13.8	69.0	645	18	US-10-653-047-4394	Sequence 4394, App	C 643	13.8	69.0	1619	16	US-10-425-114-30457	Sequence 30457, A
C 571	13.8	69.0	649	13	US-10-027-632-255429	Sequence 255429, App	C 644	13.8	69.0	1621	16	US-10-425-115-151237	Sequence 151237, App
C 572	13.8	69.0	649	15	US-10-027-632-255429	Sequence 255429, App	C 645	13.8	69.0	1669	18	US-10-739-930-4315	Sequence 4315, App
C 573	13.8	69.0	660	13	US-10-027-632-283476	Sequence 283476, App	C 646	13.8	69.0	1672	15	US-10-079-042-81	Sequence 81, Appli
C 574	13.8	69.0	660	15	US-10-027-632-283476	Sequence 283476, App	C 647	13.8	69.0	1672	15	US-10-345-820-81	Sequence 81, Appli
C 575	13.8	69.0	663	18	US-10-425-115-108281	Sequence 108281, App	C 648	13.8	69.0	1695	15	US-10-369-493-43888	Sequence 43888, A
C 576	13.8	69.0	673	16	US-10-259-194A-538	Sequence 538, App	C 649	13.8	69.0	1731	14	US-10-153-668-193	Sequence 193, App
C 577	13.8	69.0	676	13	US-10-027-632-218340	Sequence 218340, App	C 650	13.8	69.0	1756	9	US-09-193-881-11	Sequence 11, Appli
C 578	13.8	69.0	676	15	US-10-027-632-218340	Sequence 218340, App	C 651	13.8	69.0	1756	15	US-10-338-395-11	Sequence 11, Appli
C 579	13.8	69.0	693	16	US-10-282-122A-23674	Sequence 23674, A	C 652	13.8	69.0	1760	9	US-09-193-881-10	Sequence 10, Appli
C 580	13.8	69.0	697	10	US-09-890-688-99	Sequence 99, Appli	C 653	13.8	69.0	1760	15	US-10-338-395-10	Sequence 10, Appli
C 581	13.8	69.0	703	11	US-09-903-190-79	Sequence 375, App	C 654	13.8	69.0	1760	15	US-10-264-237-121	Sequence 121, App
C 582	13.8	69.0	703	11	US-09-978-360A-375	Sequence 360A-375, App	C 655	13.8	69.0	1794	15	US-10-032-585-6595	Sequence 6595, App
C 583	13.8	69.0	709	17	US-10-437-963-58671	Sequence 58671, A	C 656	13.8	69.0	1837	15	US-10-364-889-3	Sequence 3, Appli
C 584	13.8	69.0	720	16	US-10-398-221-2389	Sequence 2389, App	C 657	13.8	69.0	1837	16	US-10-038-270A-21	Sequence 21, Appli
C 585	13.8	69.0	724	13	US-10-027-632-99632	Sequence 99632, App	C 658	13.8	69.0	1850	17	US-10-433-485A-14	Sequence 14, Appli
C 586	13.8	69.0	724	15	US-10-027-632-99632	Sequence 99632, App	C 659	13.8	69.0	1850	18	US-10-855-955-3	Sequence 3, Appli
C 587	13.8	69.0	735	13	US-10-027-632-20215	Sequence 20215, A	C 660	13.8	69.0	1887	13	US-10-027-632-99970	Sequence 99970, A
588	13.8	69.0	735	15	US-10-027-632-20215	Sequence 20215, A	C 661	13.8	69.0	1887	13	US-10-027-632-99971	Sequence 99971, A
589	13.8	69.0	739	18	US-10-425-115-66578	Sequence 66578, A	C 662	13.8	69.0	1887	15	US-10-027-632-99971	Sequence 99971, A
C 590	13.8	69.0	747	9	US-09-974-300-6720	Sequence 6720, App	C 663	13.8	69.0	1917	18	US-10-425-115-66576	Sequence 66576, A
C 591	13.8	69.0	750	16	US-10-282-122A-29697	Sequence 29697, A	C 664	13.8	69.0	1917	18	US-10-739-930-1653	Sequence 1653, App
C 592	13.8	69.0	756	16	US-10-398-221-490	Sequence 490, App	C 665	13.8	69.0	1937	16	US-10-282-122A-17577	Sequence 17577, A
593	13.8	69.0	757	18	US-10-425-115-41236	Sequence 41236, A	C 666	13.8	69.0	1937	16	US-10-282-122A-17577	Sequence 17577, A
594	13.8	69.0	759	13	US-10-027-632-160987	Sequence 160987, App	C 667	13.8	69.0	1968	15	US-10-282-122A-27171	Sequence 27171, A
595	13.8	69.0	759	13	US-10-027-632-160988	Sequence 160988, App	C 668	13.8	69.0	1968	15	US-10-369-493-43817	Sequence 43817, A
596	13.8	69.0	759	15	US-10-027-632-160987	Sequence 160987, App	C 669	13.8	69.0	2000	9	US-09-938-842A-3040	Sequence 3040, App

670	13.8	69.0	2000	9	US-09-938-842A-4304	Sequence 4304, Ap	743	13.8	69.0	36159	9	US-09-749-588-3	Sequence 3, Appli
671	13.8	69.0	2000	11	US-09-938-842A-3040	Sequence 3040, Ap	744	13.8	69.0	36159	13	US-10-135-687-3	Sequence 3, Appli
672	13.8	69.0	2000	11	US-09-938-842A-4304	Sequence 4304, Ap	745	13.8	69.0	43672	13	US-10-087-193-607	Sequence 607, App
673	13.8	69.0	2019	17	US-10-437-963-22038	Sequence 22038, A	746	13.8	69.0	45774	11	US-09-984-423-311	Sequence 311, App
674	13.8	69.0	2088	17	US-10-437-963-36916	Sequence 36916, A	747	13.8	69.0	53581	13	US-10-087-193-607	Sequence 1684, App
675	13.8	69.0	2142	15	US-10-265-829-52	Sequence 52, Appli	748	13.8	69.0	63563	16	US-10-672-787-33	Sequence 33, Appl
676	13.8	69.0	2174	18	US-10-739-300-384	Sequence 384, App	749	13.8	69.0	70768	13	US-10-135-322-13	Sequence 13, Appl
677	13.8	69.0	2208	17	US-10-437-963-22039	Sequence 22039, A	750	13.8	69.0	96597	11	US-09-997-722-73	Sequence 73, Appl
678	13.8	69.0	2245	16	US-09-797-464-33	Sequence 3, Appli	751	13.8	69.0	127767	17	US-10-322-281-797	Sequence 797, App
679	13.8	69.0	2348	16	US-10-425-114-33392	Sequence 33392, A	752	13.8	69.0	131217	18	US-10-779-597-1	Sequence 1, Appli
680	13.8	69.0	2380	13	US-09-918-6249-54	Sequence 54, Appl	753	13.8	69.0	139326	17	US-10-322-281-134	Sequence 134, App
681	13.8	69.0	2380	15	US-10-177-293-442	Sequence 442, App	754	13.8	69.0	141932	15	US-10-292-798-983	Sequence 983, App
682	13.8	69.0	2380	15	US-10-172-118-946	Sequence 946, App	755	13.8	69.0	147309	9	US-09-742-312-3	Sequence 3, Appli
683	13.8	69.0	2380	15	US-10-295-027-99	Sequence 99, Appl	756	13.8	69.0	147309	15	US-10-436-185-3	Sequence 3, Appli
684	13.8	69.0	2380	16	US-10-173-999-79	Sequence 99, Appl	757	13.8	69.0	153740	17	US-10-322-696-85	Sequence 85, Appl
685	13.8	69.0	2380	16	US-10-159-563-109	Sequence 109, App	758	13.8	69.0	185548	14	US-10-175-523-62	Sequence 62, Appl
686	13.8	69.0	2380	16	US-10-342-887-946	Sequence 946, App	759	13.8	69.0	185548	14	US-10-175-523-62	Sequence 62, Appl
687	13.8	69.0	2387	15	US-10-364-237-1235	Sequence 1235, Ap	760	13.8	69.0	338702	13	US-10-087-192-292	Sequence 292, App
688	13.8	69.0	2397	15	US-10-029-386-25348	Sequence 25348, A	761	13.8	69.0	495369	16	US-10-398-221-8	Sequence 8, Appli
689	13.8	69.0	2419	18	US-10-425-115-163336	Sequence 163336, A	762	13.8	69.0	580073	15	US-10-398-221-8	Sequence 8, Appli
690	13.8	69.0	2428	16	US-10-108-260A-320	Sequence 320, App	763	13.8	69.0	684707	16	US-10-205-220-1	Sequence 1, Appli
691	13.8	69.0	2512	14	US-10-114-170-61	Sequence 61, Appl	764	13.8	69.0	1230025	16	US-10-289-762-1	Sequence 1, Appli
692	13.8	69.0	2533	16	US-10-062-674-2042	Sequence 2042, Ap	765	13.8	69.0	3186778	13	US-10-027-632-174961	Sequence 174961, A
693	13.8	69.0	2556	16	US-10-260-238-1509	Sequence 1509, Ap	766	13.8	69.0	3186778	15	US-10-027-632-174961	Sequence 174961, A
694	13.8	69.0	2560	16	US-10-424-599-51229	Sequence 51229, A	767	13.6	68.0	25	US-10-098-263B-60508	Sequence 60508, A	
695	13.8	69.0	2600	10	US-09-801-451A-1	Sequence 1, Appli	768	13.6	68.0	27	US-09-753-436-107	Sequence 107, App	
696	13.8	69.0	2629	17	US-10-467-534-98	Sequence 98, Appl	769	13.6	68.0	27	US-10-163-942-107	Sequence 107, App	
697	13.8	69.0	2629	17	US-10-437-963-36518	Sequence 36518, A	770	13.6	68.0	60	US-09-908-975-11607	Sequence 11607, A	
698	13.8	69.0	2751	16	US-10-822-122A-40306	Sequence 40306, A	771	13.6	68.0	60	US-09-908-975-23510	Sequence 23510, A	
699	13.8	69.0	2757	15	US-10-369-449-27182	Sequence 27182, A	772	13.6	68.0	116	US-09-969-373-1470	Sequence 1470, Ap	
700	13.8	69.0	2759	14	US-10-198-846-9993	Sequence 9993, Ap	773	13.6	68.0	125	US-09-864-761-20636	Sequence 20636, A	
701	13.8	69.0	2802	15	US-10-369-493-27186	Sequence 27186, A	774	13.6	68.0	156	US-10-424-599-88582	Sequence 88582, A	
702	13.8	69.0	2868	18	US-10-425-115-109792	Sequence 109792, A	775	13.6	68.0	184	US-09-864-761-18635	Sequence 18635, A	
703	13.8	69.0	2940	17	US-10-337-213-3	Sequence 3, Appli	776	13.6	68.0	185	US-10-242-535A-17713	Sequence 17713, A	
704	13.8	69.0	2992	17	US-10-437-963-67640	Sequence 67640, A	777	13.6	68.0	185	US-10-085-783A-17713	Sequence 17713, A	
705	13.8	69.0	3100	13	US-10-027-632-115302	Sequence 115302, A	778	13.6	68.0	197	US-10-424-599-18134	Sequence 18134, A	
706	13.8	69.0	3100	13	US-10-027-632-115302	Sequence 115302, A	779	13.6	68.0	201	US-10-741-601-19567	Sequence 19567, A	
707	13.8	69.0	3168	17	US-10-437-963-28825	Sequence 28825, A	780	13.6	68.0	221	US-10-425-115-93328	Sequence 93328, A	
708	13.8	69.0	3295	13	US-10-027-633-115735	Sequence 115735, A	781	13.6	68.0	225	US-10-425-115-93328	Sequence 93328, A	
709	13.8	69.0	3295	15	US-10-027-633-115735	Sequence 115735, A	782	13.6	68.0	228	US-10-424-599-1139512	Sequence 1139512, A	
710	13.8	69.0	3404	14	US-10-114-170-94	Sequence 94, Appl	783	13.6	68.0	244	US-09-736-457-386	Sequence 386, App	
711	13.8	69.0	3437	18	US-10-425-115-68961	Sequence 68961, A	784	13.6	68.0	244	US-09-902-941-386	Sequence 386, App	
712	13.8	69.0	3636	15	US-10-266-823-39	Sequence 39, Appl	785	13.6	68.0	244	US-09-849-626-386	Sequence 386, App	
713	13.8	69.0	4017	14	US-10-173-668-195	Sequence 195, App	786	13.6	68.0	244	US-09-476-300-386	Sequence 386, App	
714	13.8	69.0	4173	13	US-10-071-766-128	Sequence 128, App	787	13.6	68.0	244	US-10-017-754-386	Sequence 386, App	
715	13.8	69.0	4335	10	US-09-814-353-19950	Sequence 19950, A	788	13.6	68.0	244	US-10-113-872-386	Sequence 386, App	
716	13.8	69.0	4515	18	US-10-425-115-167184	Sequence 167184, A	789	13.6	68.0	244	US-10-283-017-386	Sequence 386, App	
717	13.8	69.0	5998	9	US-10-027-633-115735	Sequence 115735, A	790	13.6	68.0	248	US-10-424-599-140879	Sequence 140879, A	
718	13.8	69.0	6348	17	US-10-437-963-33047	Sequence 33047, A	791	13.6	68.0	265	US-09-922-293-304	Sequence 304, App	
719	13.8	69.0	7219	9	US-09-764-856-107	Sequence 107, App	792	13.6	68.0	270	US-10-425-115-120987	Sequence 120987, A	
720	13.8	69.0	7219	11	US-10-102-627-107	Sequence 107, App	793	13.6	68.0	294	US-10-425-115-32461	Sequence 32461, A	
721	13.8	69.0	7219	14	US-10-102-627-107	Sequence 107, App	794	13.6	68.0	327	US-09-895-828-197	Sequence 197, App	
722	13.8	69.0	7313	9	US-09-242-772-116	Sequence 116, App	795	13.6	68.0	327	US-10-114-666-197	Sequence 197, App	
723	13.8	69.0	8226	17	US-10-437-963-36519	Sequence 36519, A	796	13.6	68.0	340	US-10-242-535A-11634	Sequence 11634, A	
724	13.8	69.0	10254	8	US-10-158-844-29	Sequence 29, Appl	797	13.6	68.0	340	US-10-085-783A-11634	Sequence 11634, A	
725	13.8	69.0	10254	16	US-10-158-844-29	Sequence 29, Appl	798	13.6	68.0	354	US-10-404-438-14	Sequence 14, Appl	
726	13.8	69.0	13011	16	US-10-388-934-36	Sequence 36, Appl	799	13.6	68.0	360	US-10-425-115-12034	Sequence 12034, A	
727	13.8	69.0	13011	16	US-10-388-934-36	Sequence 36, Appl	800	13.6	68.0	364	US-09-918-995-30109	Sequence 30109, A	
728	13.8	69.0	13894	10	US-10-152-319A-2150	Sequence 2150, Ap	801	13.6	68.0	365	US-10-437-963-47813	Sequence 47813, A	
729	13.8	69.0	13894	16	US-09-960-870-15	Sequence 15, Appl	802	13.6	68.0	367	US-10-437-963-52754	Sequence 52754, A	
730	13.8	69.0	13894	16	US-09-960-855-15	Sequence 15, Appl	803	13.6	68.0	370	US-09-770-791-363	Sequence 363, App	
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ALIGNMENTS

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; Publication No. US20020168656A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Berish
; APPLICANT: Anderson, Sylvia
; TITLE OF INVENTION: Detection of Mutations in a Gene Encoding IKB Kinase-Complex-Associated Protein to Diagnose Familial Dysautonomia
; FILE REFERENCE: Rubin 201
; CURRENT APPLICATION NUMBER: US/10/050,189A
; CURRENT FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
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; TYPE: DNA
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US-10-050-189A-7
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; Sequence 1, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
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US-10-041-856-1
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RESULT 3
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; Sequence 514, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
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RESULT 4
US-09-796-692-299
; Sequence 299, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
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; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 299
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-299

Query Match          79.0%; Score 15.8; DB 9; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGTCGCAAAACAGTACAATG 19
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 5
US-09-796-692-453
; Sequence 453, Application US/09/796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 299
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-299

Query Match          79.0%; Score 15.8; DB 9; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGTCGCAAAACAGTACAATG 19
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 6
US-09-796-692-3607
; Sequence 3607, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
```

```

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-453

Query Match          79.0%; Score 15.8; DB 9; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGTCGCAAAACAGTACAATG 19
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 6
US-09-796-692-3607
; Sequence 3607, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
```

; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3607
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (54)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-3607

Query Match 79.0%; Score 15.8; DB 9; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||| ||||| ||||| |||||
DB 100 AGCTGCAACAGTACAATG 118

RESULT 7

US-10-040-862-299
; Sequence 299, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SEQ ID NO 299
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-10-040-862-299

Query Match 79.0%; Score 15.8; DB 14; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||| ||||| ||||| |||||
DB 100 AGCTGCAACAGTACAATG 118

RESULT 8

US-10-040-862-453
; Sequence 453, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-10-040-862-453

Query Match 79.0%; Score 15.8; DB 14; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19


```

; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3607
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(182)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-3607

Query Match          79.0%; Score 15.8; DB 16; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTCGCAAAACAGTACAAATG 19
          ||| ||||| ||||| |||
Db      100 AGCTGCAAAACAGTACAAATG 118

RESULT 13
US-10-154-884B-299

```

Sequence 2597, Application 05/10/2005-10
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander

: APPLICANT : MGate, Paul A.
 : APPLICANT : Mannion, Jane
 : APPLICANT : Retter, Marc W.
 : APPLICANT : Corixa Corporation
 : APPLICANT :

```

/ FILE OF INVENTION: REMEDIATION CARTRIDGE MANUFACTURES
/
/ FILE REFERENCE: 014058-013521US
/
/ CURRENT APPLICATION NUMBER: US 10/154,884B
/
/ CURRENT FILING DATE: 2002-05-23
/
/ PRIOR APPLICATION NUMBER: US 60/186,126
/
/ PRIOR FILING DATE: 2000-03-01
/
/ PRIOR APPLICATION NUMBER: US 60/190,479
/
/ PRIOR FILING DATE: 2000-03-17
/
/ PRIOR APPLICATION NUMBER: US 60/200,545
/
/ PRIOR FILING DATE: 2000-04-27
/
/ PRIOR APPLICATION NUMBER: US 60/200,303
/
/ PRIOR FILING DATE: 2000-04-28
/
/ PRIOR APPLICATION NUMBER: US 60/200,779
/
/ PRIOR FILING DATE: 2000-04-28
/
/ PRIOR APPLICATION NUMBER: US 60/200,999
/
/ PRIOR FILING DATE: 2000-05-01
/
/ PRIOR APPLICATION NUMBER: US 60/202,084
/
/ PRIOR FILING DATE: 2000-05-04
/
/ PRIOR APPLICATION NUMBER: US 60/206,201
/
/ PRIOR FILING DATE: 2000-05-22
/
/ PRIOR APPLICATION NUMBER: US 60/218,950
/
/ PRIOR FILING DATE: 2000-07-14
/
/ PRIOR APPLICATION NUMBER: US 60/222,903
/
/ PRIOR FILING DATE: 2000-08-03
/
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/
/ NUMBER OF SEQ ID NOS: 11290
/
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/
/ SEQ ID NO 299

```

```
/ LENGTH: 182
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(182)
/ OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-299
```

```
Query Match          79.0%; Score 15.8; DB 16; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGTCGCAAAACAGTACAATG 19
    |||
Db 100 AGCTGCAAAACAGTACAATG 118
```

RESULT 14

```
US-10-154-884B-453
/ Sequence 453, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013521US
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11290
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 453
/ LENGTH: 182
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(182)
/ OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-453
```

```
Query Match          79.0%; Score 15.8; DB 16; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGTCGCAAAACAGTACAATG 19
    |||
Db 100 AGCTGCAAAACAGTACAATG 118
```

```
Query Match          79.0%; Score 15.8; DB 16; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGTCGCAAAACAGTACAATG 19
    |||
Db 100 AGCTGCAAAACAGTACAATG 118
```

RESULT 15

```
US-10-154-884B-3607
/ Sequence 3607, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013521US
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11290
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3607
/ LENGTH: 182
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(182)
/ OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-3607
```

```
Query Match          79.0%; Score 15.8; DB 16; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGTCGCAAAACAGTACAATG 19
    |||
Db 100 AGCTGCAAAACAGTACAATG 118
```

RESULT 16

```
US-10-764-324-299
/ Sequence 299, Application US/10764324
/ Publication No. US20040175739A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Mannion, Jane
/ APPLICANT: Retter, Marc
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-013520US
/ CURRENT APPLICATION NUMBER: US/10/764,324
```

```
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 299
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-10-764-324-299
```

```
Query Match 79.0%; Score 15.8; DB 17; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 AGTCGCAACAGTCAATG 19
Db 100 AGCTGCAACAGTCAATG 118
```

```
RESULT 17
US-10-764-324-453
; Sequence 453, Application US/10/764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
```

```
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(182)
; OTHER INFORMATION: n = A,T,C or G
US-10-764-324-453
```

```
Query Match 79.0%; Score 15.8; DB 17; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 AGTCGCAACAGTCAATG 19
Db 100 AGCTGCAACAGTCAATG 118
```

```
RESULT 18
US-10-764-324-3607
; Sequence 3607, Application US/10/764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3607
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (54)
; OTHER INFORMATION: n=A,T,C or G
```

```
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
US-10-764-324-3607

Query Match      79.0%; Score 15.8; DB 17; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTCGCAACAGTACAATG 19
      || |||||
Db      100 AGCTGCAACAGTACAATG 118

RESULT 19
US-09-796-692-5819
; Sequence 5819, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/226,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5819
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (248)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (264)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-5819

Query Match      79.0%; Score 15.8; DB 9; Length 286;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTCGCAACAGTACAATG 19
      || |||||
Db      100 AGCTGCAACAGTACAATG 118
```

```
Db      100 AGCTGCAACAGTACAATG 118

RESULT 20
US-10-040-862-5819
; Sequence 5819, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5819
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (248)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (264)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-5819

Query Match      79.0%; Score 15.8; DB 14; Length 286;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTCGCAACAGTACAATG 19
      || |||||
Db      100 AGCTGCAACAGTACAATG 118

RESULT 21
US-10-057-475B-5819
; Sequence 5819, Application US/10057475B
; Publication No. US20040002068A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5819
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(286)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-5819

Query Match          79.0%; Score 15.8; DB 16; Length 286;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAAAACAGTACAATG 19
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 22
US-10-154-884B-5819
; Sequence 5819, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
```

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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5819
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(286)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-5819

Query Match          79.0%; Score 15.8; DB 16; Length 286;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAAAACAGTACAATG 19
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 23
US-10-764-324-5819
; Sequence 5819, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
```

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; FILE REFERENCE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5819
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (248)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (264)
; OTHER INFORMATION: n=A,T,C or G
US-10-764-324-5819

Query Match          79.0%; Score 15.8; DB 17; Length 286;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AGTCGCAAAACAGTACAATG 19
      ||| ||||| ||||| |||||
Db      100 AGTCGCAAAACAGTACAATG 118

RESULT 24
US-10-424-599-58096/c
; Sequence 58096, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 58096
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(395)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23473C.1
US-10-424-599-58096

Query Match          79.0%; Score 15.8; DB 16; Length 395;
Best Local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GTCGCAAAACAGTACAATGG 20
      ||| ||||| ||||| |||||
Db      331 GTAGCAAAACAGTAGAATGG 313

RESULT 25
US-09-796-692-3925
; Sequence 3925, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3925
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-3925

Query Match          79.0%; Score 15.8; DB 9; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AGTCGCAAAACAGTACAATG 19
      ||| ||||| ||||| |||||
Db      100 AGCTGCAAAACAGTACAATG 118

RESULT 26
US-09-796-692-6782
; Sequence 6782, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04

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; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6782
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6782

Query Match 79.0%; Score 15.8; DB 9; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
DB 100 AGCTGCAACAGTACAATG 118

RESULT 27
US-10-040-862-3925
; Sequence 3925, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US/10/040,862
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3925
; LENGTH: 482
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-040-862-3925

Query Match 79.0%; Score 15.8; DB 14; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
DB 100 AGCTGCAACAGTACAATG 118

RESULT 28
US-10-040-862-6782
; Sequence 6782, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6782
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6782

Query Match 79.0%; Score 15.8; DB 14; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
DB 100 AGCTGCAACAGTACAATG 118

RESULT 29
US-10-057-475B-3925
; Sequence 3925, Application US/10057475B

```
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3925
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-3925

Query Match 79.0%; Score 15.8; DB 16; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAAAACAGTACAATG 19
    ||| ||||| ||||| |||||
Db 100 AGTCGCAAAACAGTACAATG 118

RESULT 30
US-10-057-475B-6782
; Sequence 6782, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
```

```
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6782
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-6782

Query Match 79.0%; Score 15.8; DB 16; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAAAACAGTACAATG 19
    ||| ||||| ||||| |||||
Db 100 AGTCGCAAAACAGTACAATG 118

RESULT 31
US-10-154-884B-3925
; Sequence 3925, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3925

; LENGTH: 482

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-154-884B-3925

Query Match 79.0%; Score 15.8; DB 16; Length 482;

Best Local Similarity 89.5%; Pred. No. 4.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19

||| ||||| ||||| ||||| |||||

Db 100 AGCTGCAACAGTACAATG 118

RESULT 32

US-10-154-884B-6782

; Sequence 6782, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6782

; LENGTH: 482

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-154-884B-6782

Query Match 79.0%; Score 15.8; DB 16; Length 482;

Best Local Similarity 89.5%; Pred. No. 4.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19

||| ||||| ||||| ||||| |||||

Db 100 AGCTGCAACAGTACAATG 118

RESULT 33

US-10-764-324-3925

; Sequence 3925, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3925

; LENGTH: 482

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-764-324-3925

Query Match 79.0%; Score 15.8; DB 17; Length 482;

Best Local Similarity 89.5%; Pred. No. 4.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19

||| ||||| ||||| ||||| |||||

Db 100 AGCTGCAACAGTACAATG 118

RESULT 34

US-10-764-324-6782

; Sequence 6782, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6782
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-764-324-6782

Query Match      79.0%; Score 15.8; DB 17; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AGTCGCAAAACAGTACAATG 19
      ||| ||||| ||||| |||||
Db      100 AGCTGCAAAACAGTACAATG 118

RESULT 35
US-09-796-692-2741
; Sequence 2741, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2741
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-040-862-2741
```

```

; ORGANISM: Homo sapiens
; US-09-796-692-2741

Query Match      79.0%; Score 15.8; DB 9; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AGTCGCAAAACAGTACAATG 19
      ||| ||||| ||||| |||||
Db      100 AGCTGCAAAACAGTACAATG 118

RESULT 36
US-10-040-862-2741
; Sequence 2741, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520J5
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2741
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-040-862-2741

Query Match      79.0%; Score 15.8; DB 14; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AGTCGCAAAACAGTACAATG 19
      ||| ||||| ||||| |||||
Db      100 AGCTGCAAAACAGTACAATG 118

RESULT 37
US-10-057-475B-2741
; Sequence 2741, Application US/10057475B
```

```
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2741
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-2741

Query Match 79.0%; Score 15.8; DB 16; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||| ||||| ||||| |||||
Db 100 AGTCGCAACAGTACAATG 118

RESULT 38
US-10-154-884B-2741
; Sequence 2741, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2741
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-2741

Query Match 79.0%; Score 15.8; DB 16; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||| ||||| ||||| |||||
Db 100 AGTCGCAACAGTACAATG 118

RESULT 39
US-10-154-884B-2741
; Sequence 2741, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2741
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;
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-324-2741

Query Match          79.0%; Score 15.8; DB 17; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19
   |||||
Db 100 AGCTGCAAAACAGTACAATG 118

RESULT 40
US-10-029-386-13273
; Sequence 13273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13273
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR12.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EST HUMAN HIT: AI797907.1, EVALUATE 0.00e+00
; OTHER INFORMATION: NT HIT: gi13650028, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P24731, EVALUATE 8.10e+00
US-10-029-386-13273

Query Match          79.0%; Score 15.8; DB 15; Length 511;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19
   |||||
Db 301 AGCTGCAAAACAGTACAATG 319

RESULT 41
US-10-437-963-99107/c
; Sequence 99107, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 99107
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96950C.1
US-10-437-963-99107

Query Match          79.0%; Score 15.8; DB 17; Length 536;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19
   |||||
Db 231 AGTCGCAAAACAGTACAATG 213

RESULT 42
US-10-437-963-58097/c
; Sequence 58097, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 58097
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_59846C.1
US-10-437-963-58097

Query Match          79.0%; Score 15.8; DB 17; Length 1048;
Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19
   |||||
Db 945 AGTCGCAAAACAGTACAATG 927

RESULT 43
US-10-282-122A-9046
; Sequence 9046, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 60191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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RESULT 45
US-10-027-632-112288/c
; Sequence 112288, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112288
; LENGTH: 2759
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-112288

Query Match 79.0%; Score 15.8; DB 16; Length 1674;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGCGCAACAGTACAATGG 20
|||||
Db 473 GTGCGCAACATTAACAATGG 491

RESULT 44
US-09-887-576-187
; Sequence 187, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 2004
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-187

Query Match 79.0%; Score 15.8; DB 9; Length 2004;
Best Local Similarity 89.5%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
|||||
Db 419 AGITGCAACAGCAATG 437

Query Match 79.0%; Score 15.8; DB 13; Length 2759;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
|||||
Db 2559 AATGCAACAGTACAATG 2541

RESULT 46
US-10-027-632-112288/c
; Sequence 112288, Application US/10027632
; Publication No. US20020204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112288
; LENGTH: 2759
; TYPE: DNA

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; ORGANISM: Human
; US-10-027-632-112288

Query Match          79.0%; Score 15.8; DB 15; Length 2759;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTCGCAAAACAGTACAATG 19
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Db      51 AGTCGCAAAACAGCGCAATG 69

RESULT 49
US-08-961-527-170/c
; Sequence 170, Application US/08961527
; Publication No. US20020032323A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: P3340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8976 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-170

Query Match          79.0%; Score 15.8; DB 8; Length 8876;
Best Local Similarity 89.5%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCGCAAAACAGTACAATGG 20
      |||||
Db      4731 GTCGCAAAAGAGACAATGG 4713

RESULT 50
US-10-158-844-170/c
; Sequence 170, Application US/10158844
; Publication No. US20040029118A1
; GENERAL INFORMATION:
; APPLICANT: Kunsch et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:

; ORGANISM: Cryptococcus neoformans
; US-10-320-797-329

Query Match          79.0%; Score 15.8; DB 16; Length 5238;
Best Local Similarity 89.5%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCGCAAAACAGTACAATGG 20
      |||||
Db      2815 GTCGCAAAACAGTACAATGG 2797

RESULT 48
US-10-320-797-329
; Sequence 329, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Broshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 329
; LENGTH: 5238
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
; US-10-320-797-329

Query Match          79.0%; Score 15.8; DB 16; Length 5238;
Best Local Similarity 89.5%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-10-437-963-41469/c
; Sequence 41469, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41469
; LENGTH: 3546
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44810C.1
; US-10-437-963-41469

Query Match          79.0%; Score 15.8; DB 17; Length 3546;
Best Local Similarity 89.5%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCGCAAAACAGTACAATGG 20
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Db      2815 GTCGCAAAACAGTACAATGG 2797
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/ MEDIUM TYPE: CD-R
/ COMPUTER: Dell Latitude Pentium 3
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/10/158,844
/   FILING DATE: 03-Jun-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/961,527
/   FILING DATE: 1997-10-30
/   APPLICATION NUMBER: US 60/029,960
/   FILING DATE: 1996-10-31
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Hyman, Mark J.
/   REGISTRATION NUMBER: 46,789
/   REFERENCE/DOCKET NUMBER: PB340P1D1
/ INFORMATION FOR SEQ ID NO: 170:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 8876 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: double
/     TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-10-158-844-170

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Query Match      79.0%; Score 15.8; DB 16; Length 8876;
Best Local Similarity 89.5%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGCAAAACAGTACAATGG 20
      |||||
Db      4731 GTCGCAAAACAGTACAATGG 4713

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Search completed: December 3, 2004, 07:42:57
Job time : 1793.58 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 01:45:05 ; Search time 66.3158 Seconds
(without alignments)
214.365 Million cell updates/sec

Title: US-10-050-189A-7

Perfect score: 20

Sequence: 1 agtcgcaaacagtacaatgg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Capext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

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5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	79.0	906	4	US-09-583-110-2451
C 2	15.8	79.0	1281	4	US-09-583-681A-585
C 3	15.8	79.0	1704	4	US-09-328-352-890
C 4	15.8	79.0	8876	4	US-08-961-527-170
C 5	15.4	77.0	427	4	US-09-270-767-5948
C 6	15.4	77.0	427	4	US-09-270-767-21230
C 7	15.4	77.0	13086	4	US-08-956-171B-16
C 8	15.4	77.0	13086	4	US-08-781-986A-16
C 9	15.2	76.0	342	4	US-09-513-999C-34579
C 10	15.2	76.0	1278	4	US-09-328-352-2264
C 11	15.2	76.0	1278	3	US-09-134-001C-1596
C 12	15.2	76.0	1278	4	US-09-710-279-109
C 13	15.2	76.0	2335	4	US-09-026-001A-9
C 14	15.2	76.0	2359	4	US-09-026-001A-17
C 15	15.2	76.0	3172	4	US-09-710-279-3876
C 16	15.2	76.0	3172	4	US-09-710-279-4314
C 17	15.2	76.0	168575	4	US-09-426-290-1
C 18	15	75.0	4465	2	US-08-620-605D-1
C 19	15	75.0	580073	4	US-08-545-528D-1
C 20	15	75.0	580073	4	US-08-545-528D-1
C 21	14.8	74.0	192	3	US-09-134-001C-2315
C 22	14.8	74.0	272	4	US-09-270-767-2529
C 23	14.8	74.0	272	4	US-09-270-767-17811
C 24	14.8	74.0	861	4	US-09-710-279-2191
C 25	14.8	74.0	924	3	US-09-134-001C-2307
C 26	14.8	74.0	3446	4	US-09-710-279-4298
C 27	14.8	74.0	3638	4	US-09-710-279-3640

C 28	14.8	74.0	4846	4	US-09-713-273A-15
C 29	14.4	72.0	656	4	US-09-270-767-30016
C 30	14.4	72.0	724	4	US-09-270-767-13942
C 31	14.4	72.0	951	4	US-09-134-000C-875
C 32	14.4	72.0	998	3	US-09-540-014-26
C 33	14.4	72.0	1002	4	US-09-897-425-36
C 34	14.4	72.0	1002	4	US-09-897-425-37
C 35	14.4	72.0	1744	4	US-09-043-302-10
C 36	14.4	72.0	2001	4	US-09-543-681A-2598
C 37	14.4	72.0	2307	4	US-09-774-528-314
C 38	14.4	72.0	3287	4	US-09-043-302-1
C 39	14.4	72.0	3787	4	US-09-897-425-48
C 40	14.4	72.0	4545	4	US-09-897-425-53
C 41	14.4	72.0	4546	4	US-09-897-425-50
C 42	14.4	72.0	4770	3	US-09-000-094-45
C 43	14.4	72.0	4770	4	US-10-011-749-45
C 44	14.4	72.0	4770	4	US-09-000-004-45
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C 46	14.4	72.0	8010	5	PCT-US95-11859-2
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C 49	14.4	72.0	1830121	4	US-09-543-681A-1
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C 58	14.2	71.0	277	4	US-09-483-665-27
C 59	14.2	71.0	365	4	US-09-270-767-28516
C 60	14.2	71.0	501	4	US-09-134-000C-3157
C 61	14.2	71.0	554	4	US-09-621-976-1796
C 62	14.2	71.0	613	3	US-09-385-982-520
C 63	14.2	71.0	768	4	US-09-543-681A-968
C 64	14.2	71.0	998	4	US-09-270-767-12704
C 65	14.2	71.0	1119	4	US-09-543-681A-3254
C 66	14.2	71.0	1128	4	US-09-540-236-1370
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C 68	14.2	71.0	1470	4	US-09-328-352-508
C 69	14.2	71.0	2319	4	US-09-107-532A-2070
C 70	14.2	71.0	3279	4	US-09-275-608-1
C 71	14.2	71.0	4278	4	US-09-248-796A-4344
C 72	14.2	71.0	6617	4	US-09-976-594-268
C 73	14.2	71.0	9377	4	US-09-221-017B-1002
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C 75	14.2	71.0	786431	4	US-09-753-389-3
C 76	14	70.0	369	4	US-09-540-236-1310
C 77	14	70.0	405	4	US-09-540-236-1306
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C 85	13.8	69.0	411	4	US-09-583-110-2353
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C 93	13.8	69.0	607	4	US-09-910-430-2
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119	13.8	69.0	1558	3	US-09-286-691-1	Sequence 1, Appl	C 192	13.6	68.0	1317	4	US-09-270-767-12126	Sequence 12126, A
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124	13.8	69.0	1850	3	US-08-882-164D-3	Sequence 3, Appl	C 197	13.6	68.0	1554	4	US-09-489-039A-3553	Sequence 3553, App
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128	13.8	69.0	2044	4	US-09-270-767-8056	Sequence 8056, App	C 201	13.6	68.0	1750	4	US-09-495-050A-180	Sequence 180, App
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131	13.8	69.0	2251	3	US-09-453-702B-61	Sequence 61, Appl	C 204	13.6	68.0	1917	4	US-09-687-538B-3	Sequence 3, Appl
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133	13.8	69.0	2629	4	US-09-489-039A-6811	Sequence 1, Appl	C 206	13.6	68.0	2029	4	US-09-460-235B-1	Sequence 1, Appl
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136	13.8	69.0	3155	4	US-09-710-279-3424	Sequence 3424, App	C 209	13.6	68.0	2161	4	US-09-336-115C-17	Sequence 17, Appl
137	13.8	69.0	3404	3	US-09-453-702B-94	Sequence 94, Appl	C 210	13.6	68.0	2223	4	US-09-134-000C-3036	Sequence 3036, App
138	13.8	69.0	4055	4	US-09-710-279-3357	Sequence 3357, App	C 211	13.6	68.0	2248	4	US-09-336-115C-15	Sequence 15, Appl
139	13.8	69.0	10254	2	US-08-791-849A-14	Sequence 14, Appl	C 212	13.6	68.0	2298	4	US-09-650-086A-1	Sequence 1, Appl
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142	13.8	69.0	34794	4	US-10-002-720-44	Sequence 44, Appl	C 215	13.6	68.0	2418	4	US-09-586-921-52	Sequence 921, Appl
143	13.8	69.0	36159	4	US-09-749-588-3	Sequence 3, Appl	C 216	13.6	68.0	2435	4	US-09-023-655-1313	Sequence 1313, App
144	13.8	69.0	36159	4	US-10-135-687-3	Sequence 3, Appl	C 217	13.6	68.0	2547	4	US-09-221-017B-212	Sequence 212, App
145	13.8	69.0	37948	3	US-09-251-645-11	Sequence 11, Appl	C 218	13.6	68.0	2579	4	US-09-620-312D-643	Sequence 643, App
146	13.8	69.0	63563	4	US-09-596-002-33	Sequence 33, Appl	C 219	13.6	68.0	2619	4	US-09-543-681A-790	Sequence 790, App
147	13.8	69.0	580073	4	US-08-545-528D-1	Sequence 1, Appl	C 220	13.6	68.0	2647	4	US-09-220-132-77	Sequence 77, App
148	13.8	69.0	1230025	4	US-09-198-452A-1	Sequence 1, Appl	C 221	13.6	68.0	2647	5	PCT-US93-06251-77	Sequence 77, Appl
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152	13.6	68.0	27	1	US-08-483-389-107	Sequence 107, App	C 225	13.6	68.0	2875	5	PCT-US93-06251-63	Sequence 63, Appl
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154	13.6	68.0	27	2	US-08-473-503-107	Sequence 107, App	C 227	13.6	68.0	3285	4	US-09-710-279-3728	Sequence 3728, App
155	13.6	68.0	27	2	US-08-483-392-107	Sequence 107, App	C 228	13.6	68.0	3262	4	US-09-710-279-3731	Sequence 3731, App
156	13.6	68.0	27	2	US-08-720-420A-107	Sequence 107, App	C 229	13.6	68.0	3704	2	US-08-702-153-1	Sequence 1, Appl
157	13.6	68.0	27	3	US-08-714-017-107	Sequence 107, App	C 230	13.6	68.0	4041	4	US-09-710-279-3689	Sequence 3689, App
158	13.6	68.0	27	3	US-08-863-790-42	Sequence 42, Appl	C 231	13.6	68.0	4576	4	US-09-713-273A-17	Sequence 17, Appl
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165	13.6	68.0	244	4	US-09-614-124B-386	Sequence 386, App	C 238	13.6	68.0	9636	1	US-08-954-441-1	Sequence 1, Appl
166	13.6	68.0	244	4	US-09-671-325-386	Sequence 386, App	C 239	13.6	68.0	11471	3	US-09-504-358-16	Sequence 16, Appl
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168	13.6	68.0	244	4	US-09-658-824-386	Sequence 386, App	C 241	13.6	68.0	11471	4	US-10-230-562-16	Sequence 16, Appl
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171	13.6	68.0	507	4	US-09-248-796A-5866	Sequence 5866, App	C 244	13.6	68.0	26700	2	US-08-488-199-5	Sequence 5, Appl
172	13.6	68.0	507	4	US-09-248-796A-12585	Sequence 12585, A	C 245	13.6	68.0	26700	2	US-08-760-534A-1	Sequence 1, Appl
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c 310 13.2 66.0 631 3 US-08-991-789A-34 Sequence 34, Appl
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c 314 13.2 66.0 631 4 US-09-429-755-34 Sequence 34, Appl
c 315 13.2 66.0 653 4 US-09-451-651-7 Sequence 7, Appli
c 316 13.2 66.0 657 4 US-09-710-279-107 Sequence 107, Appl
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c 319 13.2 66.0 701 4 US-09-673-395A-549 Sequence 549, Appl

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C 394	13.2	66.0	2940	3	US-08-689-421-28	Sequence 28, Appl	467	13	65.0	717	4	US-09-248-796A-4471	Sequence 4471, Ap
C 395	13.2	66.0	2940	3	US-09-389-528-28	Sequence 28, Appl	468	13	65.0	717	4	US-09-248-796A-8361	Sequence 8361, Ap
C 396	13.2	66.0	2940	3	US-09-181-827A-28	Sequence 28, Appl	469	13	65.0	1015	4	US-09-743-207-5	Sequence 5, Appli
C 397	13.2	66.0	3000	4	US-09-705-267A-18	Sequence 18, Appl	470	13	65.0	1048	4	US-09-489-847-38	Sequence 38, Appl
C 398	13.2	66.0	3089	4	US-09-710-279-3965	Sequence 3965, Ap	471	13	65.0	1152	4	US-09-248-796A-6016	Sequence 6016, Ap
C 399	13.2	66.0	3197	4	US-09-710-279-3473	Sequence 3473, Ap	472	13	65.0	1343	4	US-09-270-767-13780	Sequence 13780, A
C 400	13.2	66.0	3315	4	US-09-221-017B-189	Sequence 189, App	473	13	65.0	1371	4	US-09-614-221A-405	Sequence 405, App
C 401	13.2	66.0	3429	4	US-09-710-279-3833	Sequence 383, Ap	474	13	65.0	1408	3	US-08-545-196B-11	Sequence 11, Appl
C 402	13.2	66.0	3467	3	US-08-972-719-1	Sequence 1, Appli	475	13	65.0	1408	3	US-08-545-196B-11	Sequence 11, Appl
C 403	13.2	66.0	3467	3	US-09-753-038-1	Sequence 1, Appli	476	13	65.0	1491	5	PCT-US93-18606A-20	Sequence 20, Appl
C 404	13.2	66.0	3467	3	US-09-750-175-1	Sequence 1, Appli	477	13	65.0	1582	3	US-08-545-196B-10	Sequence 10, Appl
C 405	13.2	66.0	3479	3	US-08-714-918-7	Sequence 7, Appli	478	13	65.0	1582	3	US-08-545-196B-12	Sequence 12, Appl
C 406	13.2	66.0	3479	3	US-08-625-315-7	Sequence 7, Appli	479	13	65.0	1844	4	US-09-307-973A-2	Sequence 2, Appli
C 407	13.2	66.0	3479	3	US-08-265-315-7	Sequence 7, Appli	480	13	65.0	2530	4	US-09-917-254-6	Sequence 6, Appli
C 408	13.2	66.0	3479	3	US-09-286-417-7	Sequence 7, Appli	481	13	65.0	2568	4	US-08-759-451-193	Sequence 13, App
C 409	13.2	66.0	3479	3	US-09-528-709-7	Sequence 7, Appli	482	13	65.0	2612	4	US-08-435-050A-214	Sequence 214, App
C 410	13.2	66.0	3479	3	US-09-527-745-7	Sequence 7, Appli	483	13	65.0	2703	4	US-09-482-273-101	Sequence 101, App
C 411	13.2	66.0	3514	4	US-09-710-279-3352	Sequence 3352, Ap	484	13	65.0	2709	4	US-09-482-273-101	Sequence 101, App
C 412	13.2	66.0	3836	4	US-09-976-594-55	Sequence 59, Appl	485	13	65.0	3271	3	US-08-545-196B-22	Sequence 22, Appl
C 413	13.2	66.0	4202	4	US-09-904-615-56	Sequence 56, Appl	486	13	65.0	4203	3	US-08-866-757-1	Sequence 1, Appli
C 414	13.2	66.0	4715	4	US-08-956-171B-203	Sequence 203, App	487	13	65.0	4203	3	US-09-153-593-1	Sequence 1, Appli
C 415	13.2	66.0	4715	4	US-08-781-986A-203	Sequence 203, App	488	12.8	64.0	88	3	US-08-943-731-30	Sequence 30, Appl
C 416	13.2	66.0	5194	3	US-08-844-274-16	Sequence 16, Appl	489	12.8	64.0	99	4	US-09-513-599C-30334	Sequence 30334, A
C 417	13.2	66.0	5194	3	US-08-844-274-17	Sequence 17, Appl	490	12.8	64.0	106	4	US-09-270-767-30381	Sequence 30381, A
C 418	13.2	66.0	5194	3	US-09-598-421-16	Sequence 16, Appl	491	12.8	64.0	239	4	US-09-270-767-30343	Sequence 30343, A
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C 421	13.2	66.0	5679	3	US-09-598-421-10	Sequence 10, Appl	494	12.8	64.0	269	4	US-09-513-599C-33965	Sequence 33965, A
C 422	13.2	66.0	5924	4	US-08-956-171B-130	Sequence 130, App	495	12.8	64.0	276	4	US-09-114-000C-1384	Sequence 1384, Ap
C 423	13.2	66.0	5924	4	US-08-781-986A-130	Sequence 130, App	496	12.8	64.0	285	4	US-08-313-284A-6743	Sequence 6743, Ap
C 424	13.2	66.0	6448	3	US-08-844-274-15	Sequence 15, Appl	497	12.8	64.0	292	4	US-09-513-599C-31266	Sequence 31266, A
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C 426	13.2	66.0	6741	3	US-09-794-384A-14	Sequence 14, Appl	499	12.8	64.0	307	4	US-09-702-705-375	Sequence 375, App
C 427	13.2	66.0	6743	3	US-08-937-711A-1	Sequence 1, Appli	500	12.8	64.0	307	4	US-09-702-705-588	Sequence 588, App
C 428	13.2	66.0	6743	3	US-08-224-391-83	Sequence 83, Appl	501	12.8	64.0	307	4	US-09-702-705-1271	Sequence 1271, Ap
C 429	13.2	66.0	7351	1	US-08-484-304-83	Sequence 83, Appl	502	12.8	64.0	307	4	US-09-736-457-375	Sequence 375, App
C 430	13.2	66.0	7351	1	US-08-184-009-127	Sequence 127, App	503	12.8	64.0	307	4	US-09-736-457-588	Sequence 588, App
C 431	13.2	66.0	7351	2	US-08-566-398-39	Sequence 39, Appl	504	12.8	64.0	307	4	US-09-614-124B-375	Sequence 375, App
C 432	13.2	66.0	7351	2	US-08-566-398-39	Sequence 39, Appl	505	12.8	64.0	307	4	US-09-614-124B-588	Sequence 588, App
C 433	13.2	66.0	7351	2	US-08-458-356-127	Sequence 127, App	506	12.8	64.0	307	4	US-09-614-124B-1271	Sequence 1271, Ap
C 434	13.2	66.0	7351	2	US-08-658-665-39	Sequence 39, Appl	507	12.8	64.0	307	4	US-09-671-325-375	Sequence 375, App
C 435	13.2	66.0	7351	3	US-08-786-101-3	Sequence 3, Appli	508	12.8	64.0	307	4	US-09-671-325-588	Sequence 588, App
C 436	13.2	66.0	7351	3	US-08-460-736-127	Sequence 127, App	509	12.8	64.0	307	4	US-08-671-325-1271	Sequence 1271, Ap
C 437	13.2	66.0	7351	3	US-09-085-273-39	Sequence 39, Appl	510	12.8	64.0	307	4	US-09-589-184-588	Sequence 589, App
C 438	13.2	66.0	7351	4	US-09-535-370-127	Sequence 127, App	511	12.8	64.0	307	4	US-09-589-184-588	Sequence 589, App
C 439	13.2	66.0	7351	4	US-09-916-963-39	Sequence 39, Appl	512	12.8	64.0	307	4	US-09-658-824-375	Sequence 375, App
C 440	13.2	66.0	7351	4	US-09-663-667-127	Sequence 127, App	513	12.8	64.0	307	4	US-09-658-824-588	Sequence 588, App
C 441	13.2	66.0	7560	3	US-08-844-274-20	Sequence 20, Appl	514	12.8	64.0	307	4	US-09-658-824-1271	Sequence 1271, Ap
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C 444	13.2	66.0	8340	4	US-09-874-926-4	Sequence 4, Appli	517	12.8	64.0	322	4	US-08-513-599C-2517	Sequence 2517, Ap
C 445	13.2	66.0	8921	4	US-08-956-171B-470	Sequence 470, App	518	12.8	64.0	339	4	US-09-248-796A-13167	Sequence 13167, A
C 446	13.2	66.0	8921	4	US-08-781-986A-470	Sequence 470, App	519	12.8	64.0	347	4	US-08-956-171E-1056	Sequence 1056, Ap
C 447	13.2	66.0	10726	4	US-08-961-527-66	Sequence 66, Appl	520	12.8	64.0	347	4	US-08-781-986A-1056	Sequence 1056, Ap
C 448	13.2	66.0	12614	4	US-09-577-424-1	Sequence 1, Appli	521	12.8	64.0	394	4	US-09-513-599C-12264	Sequence 12264, A
C 449	13.2	66.0	13121	4	US-08-961-527-126	Sequence 126, App	522	12.8	64.0	431	4	US-09-513-599C-10175	Sequence 10175, A
C 450	13.2	66.0	14194	4	US-09-577-424-3	Sequence 3, Appli	523	12.8	64.0	450	3	US-09-114-001C-120	Sequence 120, App
C 451	13.2	66.0	43095	4	US-09-676-519-17	Sequence 17, Appl	524	12.8	64.0	462	4	US-09-248-796A-16	Sequence 16, Appl
C 452	13.2	66.0	70000	4	US-09-851-896-3	Sequence 3, Appli	525	12.8	64.0	469	4	US-09-621-976-15549	Sequence 15549, A
C 453	13.2	66.0	84495	3	US-09-797-906-3	Sequence 3, Appli	526	12.8	64.0	486	4	US-09-270-767-8871	Sequence 8871, Ap
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C 456	13.2	66.0	168575	4	US-09-426-280-1	Sequence 1, Appli	529	12.8	64.0	487	4	US-09-736-457-1655	Sequence 1655, Ap
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C 459	13	65.0	21	4	US-09-422-978-8513	Sequence 8513, Ap	532	12.8	64.0	487	4	US-09-658-824-1655	Sequence 1655, Ap
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C 461	13	65.0	480	5	PCT-US95-04648-1	Sequence 1, Appli	534	12.8	64.0	508	4	US-09-621-976-15548	Sequence 15548, A
C 462	13	65.0	609	4	US-09-270-767-4508	Sequence 4508, Ap	535	12.8	64.0	510	4	US-09-221-017B-535	Sequence 535, App
C 463	13	65.0	609	4	US-09-270-767-19750	Sequence 19750, A	536	12.8	64.0	515	4	US-09-328-352-1453	Sequence 1453, App
C 464	13	65.0	609	4	US-09-248-796A-5067	Sequence 5067, App	537	12.8	64.0	515	4	US-09-270-767-10716	Sequence 10716, A
C 465	13	65.0	633	4	US-09-107-532A-596	Sequence 596, App	538	12.8	64.0	515	4	US-09-248-796A-2126	Sequence 2126, Ap
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c 543	12.8	64.0	731	3	US-09-328-111-438	Sequence 438, App	c 616	12.8	64.0	3006	4	US-09-710-279-3956	Sequence 1, Appli
c 544	12.8	64.0	739	4	US-09-270-767-30189	Sequence 30189, A	c 617	12.8	64.0	3083	4	US-09-710-279-4128	Sequence 3956, Ap
c 545	12.8	64.0	763	3	US-09-276-599-14	Sequence 14, Appl	c 618	12.8	64.0	3124	4	US-09-710-279-3386	Sequence 4328, Ap
c 546	12.8	64.0	763	4	US-09-598-401C-14	Sequence 14, Appl	c 619	12.8	64.0	3202	4	US-09-710-279-3386	Sequence 3386, Ap
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548	12.8	64.0	765	4	US-08-781-986A-1213	Sequence 1213, Ap	c 621	12.8	64.0	3250	1	US-07-718-575-9	Sequence 9, Appli
c 549	12.8	64.0	771	4	US-09-383-110-1452	Sequence 1452, Ap	c 622	12.8	64.0	3250	1	US-08-481-206-9	Sequence 9, Appli
c 550	12.8	64.0	780	4	US-09-540-236-192	Sequence 192, App	c 623	12.8	64.0	3250	2	US-08-486-269A-9	Sequence 9, Appli
c 551	12.8	64.0	858	4	US-09-270-767-14092	Sequence 14092, A	c 624	12.8	64.0	3292	4	US-08-620-312D-165	Sequence 165, App
c 552	12.8	64.0	927	4	US-09-328-352-3032	Sequence 3032, Ap	c 625	12.8	64.0	3318	1	US-08-336-670A-1	Sequence 1, Appli
c 553	12.8	64.0	969	4	US-09-328-352-1763	Sequence 1763, Ap	c 626	12.8	64.0	3318	3	US-08-990-470A-1	Sequence 1, Appli
c 554	12.8	64.0	975	4	US-09-710-279-2623	Sequence 2623, Ap	c 627	12.8	64.0	3318	3	US-08-817-707-1	Sequence 1, Appli
c 555	12.8	64.0	1001	4	US-09-641-638-257	Sequence 257, App	c 628	12.8	64.0	3319	3	US-08-537-361E-1	Sequence 1, Appli
c 556	12.8	64.0	1001	4	US-10-170-097-257	Sequence 257, App	c 629	12.8	64.0	3561	3	US-09-134-001C-1685	Sequence 1685, Ap
c 557	12.8	64.0	1023	4	US-09-328-352-3000	Sequence 3000, Ap	c 630	12.8	64.0	3636	1	US-07-753-520B-1	Sequence 1, Appli
c 558	12.8	64.0	1045	4	US-09-270-767-14219	Sequence 14219, A	c 631	12.8	64.0	4500	1	US-08-468-557-3	Sequence 3, Appli
c 559	12.8	64.0	1083	4	US-09-134-000C-2381	Sequence 2381, Ap	c 632	12.8	64.0	4512	4	US-09-792-616-2	Sequence 2, Appli
c 560	12.8	64.0	1098	4	US-09-270-767-18597	Sequence 3315, Ap	c 633	12.8	64.0	4527	1	US-07-621-193A-1	Sequence 1, Appli
c 561	12.8	64.0	1098	4	US-09-270-767-18597	Sequence 18597, A	c 634	12.8	64.0	4527	1	US-08-018-489C-1	Sequence 1, Appli
c 562	12.8	64.0	1116	3	US-08-134-001C-906	Sequence 906, App	c 635	12.8	64.0	4748	4	US-08-426-630-29	Sequence 29, Appli
c 563	12.8	64.0	1154	3	US-09-774-528-333	Sequence 333, App	c 636	12.8	64.0	4980	4	US-09-752-616-8	Sequence 8, Appli
c 564	12.8	64.0	1201	4	US-09-023-655-552	Sequence 552, App	c 637	12.8	64.0	5499	3	US-08-479-722B-1	Sequence 1, Appli
c 565	12.8	64.0	1230	4	US-09-270-767-6928	Sequence 6928, Ap	c 638	12.8	64.0	5499	4	US-09-592-685-1	Sequence 1, Appli
c 566	12.8	64.0	1278	4	US-09-270-767-22210	Sequence 22210, A	c 639	12.8	64.0	5502	5	PCT-US95-03251-17	Sequence 17, Appli
c 567	12.8	64.0	1278	4	US-09-543-681A-1870	Sequence 1870, Ap	c 640	12.8	64.0	6386	2	US-08-483-376-1	Sequence 1, Appli
c 568	12.8	64.0	1299	4	US-09-620-312D-659	Sequence 659, App	c 641	12.8	64.0	6414	3	US-08-134-001C-1626	Sequence 1626, Ap
c 569	12.8	64.0	1306	4	US-09-270-767-14251	Sequence 14251, A	c 642	12.8	64.0	7650	2	US-08-867-941-1	Sequence 1, Appli
c 570	12.8	64.0	1350	4	US-09-023-655-1	Sequence 1, Appli	c 643	12.8	64.0	7650	3	US-09-074-658-1	Sequence 1, Appli
c 571	12.8	64.0	1368	4	US-09-543-681A-2871	Sequence 2871, Ap	c 644	12.8	64.0	8268	1	US-08-375-709-10	Sequence 10, Appli
c 572	12.8	64.0	1428	4	US-09-614-912-23	Sequence 23, Appli	c 645	12.8	64.0	8268	1	US-08-752-929-10	Sequence 10, Appli
c 573	12.8	64.0	1431	4	US-09-328-352-2609	Sequence 2609, Ap	c 646	12.8	64.0	8268	4	US-09-231-899-83	Sequence 83, Appli
c 574	12.8	64.0	1437	4	US-09-248-796A-9985	Sequence 9985, Ap	c 647	12.8	64.0	9578	4	US-08-961-527-127	Sequence 127, App
c 575	12.8	64.0	1455	4	US-09-540-236-1578	Sequence 1578, Ap	c 648	12.8	64.0	17310	4	US-08-956-171E-23	Sequence 23, Appli
c 576	12.8	64.0	1455	4	US-10-142-231-43	Sequence 43, Appli	c 649	12.8	64.0	17310	4	US-08-781-986A-23	Sequence 23, Appli
c 577	12.8	64.0	1458	4	US-09-543-681A-3271	Sequence 3271, Ap	c 650	12.8	64.0	18073	3	US-08-078-294-12	Sequence 12, Appli
c 578	12.8	64.0	1524	4	US-09-248-796A-5061	Sequence 5061, Ap	c 651	12.8	64.0	18073	3	US-08-943-731-1	Sequence 1, Appli
c 579	12.8	64.0	1528	1	US-08-288-899-1	Sequence 1, Appli	c 652	12.8	64.0	37030	4	US-08-311-731A-25	Sequence 25, Appli
c 580	12.8	64.0	1528	1	US-08-288-899-3	Sequence 3, Appli	c 653	12.8	64.0	37895	1	US-08-375-709-1	Sequence 1, Appli
c 581	12.8	64.0	1528	1	US-08-471-206-1	Sequence 1, Appli	c 654	12.8	64.0	37895	1	US-08-752-929-1	Sequence 1, Appli
c 582	12.8	64.0	1528	1	US-08-471-206-5	Sequence 5, Appli	c 655	12.8	64.0	37895	3	US-09-090-793-1	Sequence 1, Appli
c 583	12.8	64.0	1528	1	US-08-481-025D-1	Sequence 1, Appli	c 656	12.8	64.0	37895	4	US-09-231-899-1	Sequence 1, Appli
c 584	12.8	64.0	1547	1	US-08-288-899-4	Sequence 4, Appli	c 657	12.8	64.0	42571	4	US-08-810-347-3	Sequence 3, Appli
c 585	12.8	64.0	1547	1	US-08-471-206-8	Sequence 8, Appli	c 658	12.8	64.0	49617	4	US-09-596-002-28	Sequence 28, Appli
c 586	12.8	64.0	1557	4	US-09-710-279-505	Sequence 505, App	c 659	12.8	64.0	107820	4	US-09-792-616-1	Sequence 16, Appli
c 587	12.8	64.0	1581	4	US-09-800-729-22	Sequence 22, Appli	c 660	12.8	64.0	152331	3	US-09-128-155-16	Sequence 17, Appli
c 588	12.8	64.0	1584	3	US-09-134-001C-1528	Sequence 1528, Ap	c 661	12.8	64.0	176373	3	US-09-128-155-17	Sequence 2, Appli
c 589	12.8	64.0	1623	4	US-09-107-532A-1813	Sequence 1813, Ap	c 662	12.8	64.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 590	12.8	64.0	1633	4	US-10-140-002-217	Sequence 217, App	c 663	12.8	64.0	4411529	3	US-09-103-840A-1	Sequence 32, Appli
c 591	12.8	64.0	1668	4	US-09-543-681A-3706	Sequence 3706, Ap	c 664	12.6	63.0	36	1	US-08-433-010-32	Sequence 108, App
c 592	12.8	64.0	1734	4	US-09-543-681A-4053	Sequence 4053, Ap	c 665	12.6	63.0	36	1	US-08-482-882-108	Sequence 108, App
c 593	12.8	64.0	1750	4	US-08-956-171E-728	Sequence 728, App	c 666	12.6	63.0	36	1	US-08-483-389-108	Sequence 108, App
c 594	12.8	64.0	1750	4	US-08-781-986A-728	Sequence 728, App	c 667	12.6	63.0	36	2	US-08-487-113D-108	Sequence 108, App
c 595	12.8	64.0	1757	4	US-10-116-993A-2	Sequence 2, Appli	c 668	12.6	63.0	36	2	US-08-473-503-108	Sequence 108, App
c 596	12.8	64.0	1785	5	PCT-US94-22912-1	Sequence 1, Appli	c 669	12.6	63.0	36	2	US-08-483-932-108	Sequence 108, App
c 597	12.8	64.0	1845	4	US-09-489-039A-5434	Sequence 5434, Ap	c 670	12.6	63.0	36	2	US-08-720-420A-108	Sequence 108, App
c 598	12.8	64.0	1847	4	US-09-221-017B-998	Sequence 998, App	c 671	12.6	63.0	36	3	US-08-714-017-108	Sequence 108, App
c 599	12.8	64.0	2014	1	US-07-798-776-1	Sequence 1, Appli	c 672	12.6	63.0	36	3	US-08-863-790-43	Sequence 43, Appli
c 600	12.8	64.0	2014	3	US-08-251-288A-1	Sequence 1, Appli	c 673	12.6	63.0	36	3	US-08-475-680-108	Sequence 108, App
c 601	12.8	64.0	2014	3	US-09-298-819A-1	Sequence 1, Appli	c 674	12.6	63.0	36	3	US-08-296-749-43	Sequence 43, Appli
c 602	12.8	64.0	2014	4	US-09-586-563C-1	Sequence 1, Appli	c 675	12.6	63.0	36	3	US-08-218-369-13	Sequence 13, Appli
c 603	12.8	64.0	2014	4	US-09-386-562C-1	Sequence 1, Appli	c 676	12.6	63.0	36	3	US-08-218-369-18	Sequence 18, Appli
c 604	12.8	64.0	2051	4	US-09-636-215-699	Sequence 699, App	c 677	12.6	63.0	36	4	US-09-904-599A-13	Sequence 13, Appli
c 605	12.8	64.0	2051	4	US-09-685-166A-699	Sequence 699, App	c 678	12.6	63.0	36	5	PCT-US95-03742-13	Sequence 13, Appli
c 606	12.8	64.0	2051	4	US-09-679-426-699	Sequence 699, App	c 679	12.6	63.0	36	5	PCT-US95-03742-18	Sequence 18, Appli
c 607	12.8	64.0	2822	3	US-08-810-009-3	Sequence 3, Appli	c 680	12.6	63.0	57	3	US-09-275-850-236	Sequence 236, App
c 608	12.8	64.0	2822	4	US-09-776-490-3	Sequence 3, Appli	c 681	12.6	63.0	60	3	US-08-870-930-52	Sequence 52, Appli
c 609	12.8	64.0	2835	3	US-09-134-001C-1515	Sequence 1515, Ap	c 682	12.6	63.0	60	4	US-08-254-968-55	Sequence 55, Appli
c 610	12.8	64.0	2866	4	US-09-328-352-3232	Sequence 3232, Ap	c 683	12.6	63.0	83	4	US-09-792-024-188	Sequence 188, App
c 611	12.8	64.0	2955	2	US-08-867-941-4	Sequence 4, Appli	c 684	12.6	63.0	88	1	US-08-433-126A-68	Sequence 68, Appli

C 685	12.6	63.0	88	1	US-08-433-124A-68	Sequence 68, Appl	758	12.6	63.0	636	4	US-09-248-796A-1447	Sequence 1447, Ap
C 686	12.6	63.0	88	3	US-08-976-413A-68	Sequence 68, Appl	759	12.6	63.0	655	1	US-08-397-602A-7	Sequence 7, Appl
C 687	12.6	63.0	88	5	FCT-US96-06059-68	Sequence 68, Appl	760	12.6	63.0	655	4	US-08-270-767-620	Sequence 620, App
C 688	12.6	63.0	110	4	US-09-513-999C-29302	Sequence 29302, A	761	12.6	63.0	655	4	US-08-270-767-15902	Sequence 15902, A
C 689	12.6	63.0	119	4	US-09-513-999C-34580	Sequence 34580, A	762	12.6	63.0	663	4	US-09-252-991A-9870	Sequence 9870, Ap
C 690	12.6	63.0	148	3	US-09-488-799-84	Sequence 84, Appl	763	12.6	63.0	672	4	US-09-710-279-2823	Sequence 2823, Ap
C 691	12.6	63.0	167	3	US-08-512-861A-14	Sequence 14, Appl	764	12.6	63.0	681	3	US-09-134-001C-2410	Sequence 2410, Ap
C 692	12.6	63.0	186	4	US-09-248-796A-7489	Sequence 7489, Ap	765	12.6	63.0	693	3	US-08-543-246B-13	Sequence 13, Appl
C 693	12.6	63.0	201	4	US-09-134-000C-200	Sequence 200, App	766	12.6	63.0	700	3	US-08-270-767-13663	Sequence 13663, A
C 694	12.6	63.0	220	4	US-09-270-767-7444	Sequence 7444, Ap	767	12.6	63.0	711	2	US-08-485-380-9	Sequence 9, Appl
C 695	12.6	63.0	220	4	US-09-270-767-22726	Sequence 22726, A	768	12.6	63.0	711	2	US-08-480-478-38	Sequence 38, Appl
C 696	12.6	63.0	228	4	US-09-107-532A-426	Sequence 426, App	769	12.6	63.0	711	2	US-08-486-397-9	Sequence 9, Appl
C 697	12.6	63.0	229	4	US-09-513-999C-9015	Sequence 9015, Ap	770	12.6	63.0	711	2	US-08-486-399-9	Sequence 9, Appl
C 698	12.6	63.0	237	4	US-09-248-796A-9383	Sequence 9383, Ap	771	12.6	63.0	711	2	US-08-461-965-9	Sequence 9, Appl
C 699	12.6	63.0	253	4	US-09-513-999C-33495	Sequence 33495, A	772	12.6	63.0	711	2	US-08-326-110A-38	Sequence 38, Appl
C 700	12.6	63.0	266	4	US-08-554-133-532	Sequence 532, App	773	12.6	63.0	711	2	US-08-634-641-9	Sequence 9, Appl
C 701	12.6	63.0	273	2	US-08-611-757-59	Sequence 99, Appl	774	12.6	63.0	711	3	US-08-249-471-9	Sequence 9, Appl
C 702	12.6	63.0	273	5	FCT-US95-05980-99	Sequence 99, Appl	775	12.6	63.0	711	3	US-08-249-472-9	Sequence 9, Appl
C 703	12.6	63.0	279	4	US-09-313-294A-2462	Sequence 2462, Ap	776	12.6	63.0	711	3	US-08-249-451-9	Sequence 9, Appl
C 704	12.6	63.0	291	4	US-09-513-999C-35779	Sequence 35779, A	777	12.6	63.0	711	3	US-08-809-455-9	Sequence 9, Appl
C 705	12.6	63.0	301	4	US-09-270-767-7825	Sequence 7825, Ap	778	12.6	63.0	711	3	US-09-249-461-9	Sequence 9, Appl
C 706	12.6	63.0	301	4	US-09-270-767-23107	Sequence 23107, A	779	12.6	63.0	711	3	US-09-249-448-9	Sequence 9, Appl
C 707	12.6	63.0	312	4	US-09-513-999C-846	Sequence 846, App	780	12.6	63.0	711	4	US-09-249-473-9	Sequence 9, Appl
C 708	12.6	63.0	316	4	US-09-358-055B-146	Sequence 146, App	781	12.6	63.0	715	4	US-08-780-113D-27	Sequence 27, Appl
C 709	12.6	63.0	319	4	US-09-513-999C-25599	Sequence 25599, A	782	12.6	63.0	723	4	US-08-248-796A-14	Sequence 14, Appl
C 710	12.6	63.0	336	4	US-09-252-991A-1232	Sequence 1232, Ap	783	12.6	63.0	744	4	US-09-107-532A-317	Sequence 317, App
C 711	12.6	63.0	339	4	US-09-248-796A-8909	Sequence 8909, Ap	784	12.6	63.0	750	3	US-08-488-123-11	Sequence 11, Appl
C 712	12.6	63.0	349	4	US-09-621-976-1528	Sequence 1528, Ap	785	12.6	63.0	750	4	US-08-488-123-11	Sequence 11, Appl
C 713	12.6	63.0	357	4	US-09-621-976-1554	Sequence 1554, Ap	786	12.6	63.0	771	4	US-09-270-767-13629	Sequence 13629, A
C 714	12.6	63.0	364	4	US-09-621-976-18582	Sequence 18582, A	787	12.6	63.0	790	4	US-09-614-912-45	Sequence 45, Appl
C 715	12.6	63.0	370	4	US-09-358-055B-145	Sequence 145, App	788	12.6	63.0	807	4	US-05-540-336-83	Sequence 83, Appl
C 716	12.6	63.0	375	4	US-09-513-999C-1244	Sequence 1244, Ap	789	12.6	63.0	807	4	US-05-583-110-1643	Sequence 1643, Ap
C 717	12.6	63.0	387	4	US-09-248-796A-781	Sequence 781, App	790	12.6	63.0	810	4	US-09-270-767-6590	Sequence 6590, A
C 718	12.6	63.0	396	4	US-09-358-055B-134	Sequence 134, App	791	12.6	63.0	810	4	US-09-270-767-21872	Sequence 21872, A
C 719	12.6	63.0	401	4	US-09-643-597-269	Sequence 269, App	792	12.6	63.0	819	4	US-09-710-279-3197	Sequence 3197, A
C 720	12.6	63.0	401	4	US-09-480-884B-269	Sequence 269, App	793	12.6	63.0	822	4	US-09-248-796A-7126	Sequence 7126, Ap
C 721	12.6	63.0	401	4	US-09-542-615A-269	Sequence 269, App	794	12.6	63.0	825	3	US-09-134-001C-849	Sequence 849, App
C 722	12.6	63.0	401	4	US-09-606-421B-269	Sequence 269, App	795	12.6	63.0	838	3	US-09-134-001C-849	Sequence 849, App
C 723	12.6	63.0	401	4	US-09-630-940B-269	Sequence 269, App	796	12.6	63.0	887	4	US-09-122-400B-21	Sequence 21, Appl
C 724	12.6	63.0	430	4	US-09-270-767-4030	Sequence 4030, Ap	797	12.6	63.0	887	4	US-09-270-767-17258	Sequence 17258, Ap
C 725	12.6	63.0	430	4	US-09-270-767-19312	Sequence 19312, A	798	12.6	63.0	894	4	US-09-540-236-1376	Sequence 1376, Ap
C 726	12.6	63.0	442	3	US-09-270-767-357-132	Sequence 132, App	799	12.6	63.0	900	4	US-09-134-000C-2283	Sequence 2283, Ap
C 727	12.6	63.0	443	4	US-09-281-646B-28	Sequence 28, Appl	800	12.6	63.0	908	3	US-09-439-313-350	Sequence 350, App
C 728	12.6	63.0	443	4	US-09-621-976-15285	Sequence 15285, A	801	12.6	63.0	908	3	US-09-352-616A-350	Sequence 350, App
C 729	12.6	63.0	453	4	US-09-513-999C-3803	Sequence 3803, Ap	802	12.6	63.0	908	4	US-08-636-315-350	Sequence 350, App
C 730	12.6	63.0	464	4	US-09-358-055B-144	Sequence 144, App	803	12.6	63.0	908	4	US-08-685-166A-350	Sequence 350, App
C 731	12.6	63.0	471	4	US-09-621-976-13631	Sequence 13631, A	804	12.6	63.0	918	4	US-09-679-426-350	Sequence 350, App
C 732	12.6	63.0	489	4	US-09-543-681A-3833	Sequence 3833, Ap	805	12.6	63.0	924	3	US-09-489-039A-7166	Sequence 7166, Ap
C 733	12.6	63.0	492	4	US-09-248-796A-12083	Sequence 12083, A	806	12.6	63.0	927	4	US-09-134-001C-1196	Sequence 1196, Ap
C 734	12.6	63.0	499	4	US-09-621-976-2213	Sequence 2213, Ap	807	12.6	63.0	927	4	US-09-248-796A-269	Sequence 269, App
C 735	12.6	63.0	503	4	US-09-495-050A-69	Sequence 69, Appl	808	12.6	63.0	936	2	US-09-543-681A-523	Sequence 523, App
C 736	12.6	63.0	504	4	US-09-543-681A-1716	Sequence 1716, Ap	809	12.6	63.0	936	2	US-08-557-309B-9	Sequence 9, Appl
C 737	12.6	63.0	522	4	US-09-637-746-7	Sequence 7, Appl	810	12.6	63.0	936	3	US-08-834-306-9	Sequence 9, Appl
C 738	12.6	63.0	526	4	US-09-270-767-91	Sequence 91, Appl	811	12.6	63.0	936	3	US-08-993-674A-9	Sequence 9, Appl
C 739	12.6	63.0	526	4	US-09-270-767-15373	Sequence 15373, A	812	12.6	63.0	945	4	US-09-256-976-9	Sequence 9, Appl
C 740	12.6	63.0	528	4	US-09-107-532A-2999	Sequence 2999, Ap	813	12.6	63.0	945	4	US-09-543-681A-3238	Sequence 3238, Ap
C 741	12.6	63.0	543	4	US-09-252-991A-5578	Sequence 5578, Ap	814	12.6	63.0	950	4	US-09-371-307-6	Sequence 6, Appl
C 742	12.6	63.0	560	4	US-09-270-767-3421	Sequence 3421, Ap	815	12.6	63.0	956	4	US-08-956-171E-687	Sequence 687, App
C 743	12.6	63.0	560	4	US-09-270-767-18703	Sequence 18703, A	816	12.6	63.0	956	4	US-08-781-986A-687	Sequence 687, App
C 744	12.6	63.0	564	4	US-09-248-796A-2132	Sequence 2132, Ap	817	12.6	63.0	963	4	US-08-270-767-14606	Sequence 14606, A
C 745	12.6	63.0	572	4	US-09-270-767-2005	Sequence 2005, Ap	818	12.6	63.0	1002	4	US-09-641-638-591	Sequence 591, App
C 746	12.6	63.0	572	4	US-09-270-767-17287	Sequence 17287, A	819	12.6	63.0	1002	4	US-10-170-097-591	Sequence 591, App
C 747	12.6	63.0	585	4	US-09-270-767-824	Sequence 824, App	820	12.6	63.0	1020	2	US-07-757-606B-3	Sequence 3, Appl
C 748	12.6	63.0	585	4	US-09-270-767-16106	Sequence 16106, A	821	12.6	63.0	1020	2	US-07-757-606B-7	Sequence 7, Appl
C 749	12.6	63.0	588	4	US-09-543-681A-2993	Sequence 2993, Ap	822	12.6	63.0	1020	4	US-09-543-681A-2739	Sequence 2739, Ap
C 750	12.6	63.0	600	4	US-09-669-751-170	Sequence 170, App	823	12.6	63.0	1056	4	US-09-602-787A-271	Sequence 271, App
C 751	12.6	63.0	600	4	US-09-252-991A-5650	Sequence 5650, Ap	824	12.6	63.0	1083	4	US-08-543-681A-384	Sequence 384, Ap
C 752	12.6	63.0	630	4	US-09-543-681A-3798	Sequence 3798, Ap	825	12.6	63.0	1089	4	US-09-540-236-323	Sequence 323, App
C 753	12.6	63.0	631	3	US-09-439-313-446	Sequence 446, App	826	12.6	63.0	1104	4	US-09-489-039A-575	Sequence 575, App
C 754	12.6	63.0	631	3	US-09-352-616A-446	Sequence 446, App	827	12.6	63.0	1110	1	US-08-257-073-11	Sequence 11, Appl
C 755	12.6	63.0	631	4	US-09-636-215-446	Sequence 446, App	828	12.6	63.0	1113	4	US-09-107-532A-1337	Sequence 1337, Ap
C 756	12.6	63.0	631	4	US-09-685-166A-446	Sequence 446, App	829	12.6	63.0	1122	2	US-08-820-170A-26	Sequence 26, Appl
C 757	12.6	63.0	631	4	US-09-679-426-446	Sequence 446, App	830	12.6	63.0	1122	3	US-09-055-699-26	Sequence 26, Appl

831	12.6	63.0	1122	3	US-09-273-565-26	Sequence 26, Appl	904	12.6	63.0	1695	4	US-09-489-039A-6876	Sequence 6876, Ap
832	12.6	63.0	1122	3	US-09-365-538-26	Sequence 26, Appl	905	12.6	63.0	1695	4	US-09-227-853A-1	Sequence 1, Appl
833	12.6	63.0	1122	3	US-09-661-468-26	Sequence 26, Appl	906	12.6	63.0	1695	5	PCT-US95-06385-1	Sequence 1, Appl
834	12.6	63.0	1122	3	US-09-376-165-26	Sequence 26, Appl	907	12.6	63.0	1721	2	US-08-820-170A-27	Sequence 27, Appl
835	12.6	63.0	1131	2	US-08-758-621-9	Sequence 9, Appl	908	12.6	63.0	1721	3	US-09-055-699-27	Sequence 27, Appl
836	12.6	63.0	1131	2	US-09-107-858-9	Sequence 9, Appl	909	12.6	63.0	1721	3	US-09-273-565-27	Sequence 27, Appl
837	12.6	63.0	1131	4	US-09-579-174-9	Sequence 9, Appl	910	12.6	63.0	1721	3	US-09-565-538-27	Sequence 27, Appl
838	12.6	63.0	1140	1	US-08-322-677A-11	Sequence 11, Appl	911	12.6	63.0	1721	3	US-08-681-468-27	Sequence 27, Appl
839	12.6	63.0	1140	1	US-08-322-677A-12	Sequence 12, Appl	912	12.6	63.0	1721	4	US-08-976-165-27	Sequence 27, Appl
840	12.6	63.0	1140	1	US-08-322-676-11	Sequence 11, Appl	c 913	12.6	63.0	1799	4	US-09-222-938A-24	Sequence 24, Appl
841	12.6	63.0	1140	1	US-08-322-676-12	Sequence 12, Appl	914	12.6	63.0	1806	4	US-09-746-359A-36	Sequence 36, Appl
842	12.6	63.0	1140	3	US-08-898-218-11	Sequence 11, Appl	915	12.6	63.0	1833	4	US-09-248-796A-2927	Sequence 2927, Ap
843	12.6	63.0	1140	3	US-08-898-218-12	Sequence 12, Appl	916	12.6	63.0	1866	3	US-09-173-581-13	Sequence 13, Appl
844	12.6	63.0	1140	3	US-08-848-793-11	Sequence 11, Appl	917	12.6	63.0	1866	3	US-09-420-915-13	Sequence 13, Appl
845	12.6	63.0	1140	3	US-08-848-793-12	Sequence 12, Appl	c 918	12.6	63.0	1875	4	US-09-543-681A-171	Sequence 171, Appl
846	12.6	63.0	1140	3	US-09-445-270-6	Sequence 6, Appl	919	12.6	63.0	1887	4	US-08-841-786-12	Sequence 12, Appl
847	12.6	63.0	1140	3	US-09-445-270-8	Sequence 8, Appl	c 920	12.6	63.0	1888	4	US-09-665-189A-65	Sequence 65, Appl
848	12.6	63.0	1140	3	US-08-322-678-11	Sequence 11, Appl	921	12.6	63.0	1894	4	US-09-710-279-4364	Sequence 4364, Ap
849	12.6	63.0	1140	4	US-08-322-678-12	Sequence 12, Appl	922	12.6	63.0	1941	4	US-09-976-594-996	Sequence 996, App
850	12.6	63.0	1143	3	US-08-369-050-1	Sequence 1, Appl	c 923	12.6	63.0	1953	4	US-09-252-991A-10725	Sequence 10725, A
851	12.6	63.0	1143	6	5336611-1	Patent No. 5336611	924	12.6	63.0	1953	4	US-09-543-681A-3542	Sequence 3542, Ap
852	12.6	63.0	1146	3	US-08-596-684P-1	Sequence 1, Appl	925	12.6	63.0	1962	4	US-09-540-236-425	Sequence 425, App
853	12.6	63.0	1146	3	US-09-448-796A-6803	Sequence 6803, Ap	926	12.6	63.0	1962	4	US-09-919-039-376	Sequence 376, App
854	12.6	63.0	1149	4	US-09-492-709A-139	Sequence 139, App	927	12.6	63.0	1990	3	US-08-858-207A-87	Sequence 87, Appl
855	12.6	63.0	1164	4	US-09-295-593-35	Sequence 35, Appl	928	12.6	63.0	2019	3	US-09-345-214-15	Sequence 15, Appl
856	12.6	63.0	1173	4	US-09-328-352-787	Sequence 787, App	929	12.6	63.0	2019	4	US-09-743-980-15	Sequence 15, Appl
857	12.6	63.0	1173	4	US-09-710-279-1421	Sequence 1421, Ap	c 930	12.6	63.0	2208	4	US-09-248-796A-4999	Sequence 4999, Ap
858	12.6	63.0	1188	4	US-09-134-000C-2036	Sequence 2036, Ap	c 931	12.6	63.0	2250	4	US-09-583-110-260	Sequence 260, App
859	12.6	63.0	1195	3	US-08-890-719-10	Sequence 10, Appl	c 932	12.6	63.0	2259	4	US-09-710-279-4078	Sequence 4078, Ap
860	12.6	63.0	1197	3	US-08-890-719-7	Sequence 7, Appl	c 933	12.6	63.0	2275	4	US-09-281-646B-1	Sequence 1, Appl
861	12.6	63.0	1197	4	US-09-352-991A-6737	Sequence 6737, Ap	934	12.6	63.0	2280	1	US-07-661-378A-1	Sequence 1, Appl
862	12.6	63.0	1200	4	US-09-270-767-2780A	Sequence 2780A, A	935	12.6	63.0	2280	1	US-07-918-318-1	Sequence 1, Appl
863	12.6	63.0	1209	4	US-08-956-171E-462	Sequence 462, App	936	12.6	63.0	2280	2	US-08-413-724-1	Sequence 1, Appl
864	12.6	63.0	1209	4	US-08-781-986A-462	Sequence 462, App	937	12.6	63.0	2280	3	US-08-853-494-1	Sequence 1, Appl
865	12.6	63.0	1222	3	US-08-543-246B-5	Sequence 5, Appl	938	12.6	63.0	2345	4	US-09-252-931A-6782	Sequence 6782, Ap
866	12.6	63.0	1223	4	US-09-016-434-1347	Sequence 1347, Ap	c 939	12.6	63.0	2355	3	US-08-086-143B-1	Sequence 1, Appl
867	12.6	63.0	1230	3	US-08-890-719-6	Sequence 6, Appl	c 940	12.6	63.0	2355	5	PCT-US92-10621-1	Sequence 1, Appl
868	12.6	63.0	1236	4	US-09-328-352-1558	Sequence 1558, Ap	c 941	12.6	63.0	2355	5	PCT-US94-02233-1	Sequence 1, Appl
869	12.6	63.0	1239	4	US-09-710-279-367	Sequence 367, App	942	12.6	63.0	2370	4	US-09-252-991A-10440	Sequence 10440, A
870	12.6	63.0	1248	4	US-09-540-236-680	Sequence 680, App	943	12.6	63.0	2403	4	US-09-614-912-23	Sequence 23, Appl
871	12.6	63.0	1260	4	US-09-270-767-2001	Sequence 2001, Ap	944	12.6	63.0	2418	4	US-09-543-681A-3728	Sequence 3728, Ap
872	12.6	63.0	1260	4	US-09-270-767-17283	Sequence 17283, A	c 945	12.6	63.0	2451	1	US-07-731-157A-3	Sequence 3, Appl
873	12.6	63.0	1260	4	US-09-448-796A-2943	Sequence 2943, Ap	c 946	12.6	63.0	2451	1	US-08-229-444B-1	Sequence 1, Appl
874	12.6	63.0	1263	4	US-09-107-532A-352	Sequence 352, App	c 947	12.6	63.0	2451	2	US-08-541-780-3	Sequence 3, Appl
875	12.6	63.0	1263	4	US-09-489-039A-6703	Sequence 6703, Ap	948	12.6	63.0	2458	4	US-09-919-039-145	Sequence 145, App
876	12.6	63.0	1272	4	US-09-252-991A-6952	Sequence 6952, Ap	c 949	12.6	63.0	2508	4	US-09-248-796A-971	Sequence 971, App
877	12.6	63.0	1275	4	US-09-915-182-1	Sequence 1, Appl	950	12.6	63.0	2624	4	US-09-270-767-26401	Sequence 26401, A
878	12.6	63.0	1287	4	US-09-328-352-1741	Sequence 1741, Ap	c 951	12.6	63.0	2625	3	US-09-245-041-18	Sequence 18, Appl
879	12.6	63.0	1310	4	US-09-501-115-19	Sequence 19, Appl	c 952	12.6	63.0	2625	4	US-09-358-055B-18	Sequence 18, Appl
880	12.6	63.0	1320	6	5217878-1	Patent No. 5217878	c 953	12.6	63.0	2625	4	US-08-893-238-18	Sequence 18, Appl
881	12.6	63.0	1326	4	US-09-489-039A-3441	Sequence 3441, Ap	954	12.6	63.0	2739	4	US-09-348-352-1197	Sequence 1197, Ap
882	12.6	63.0	1328	4	US-09-482-273-84	Sequence 84, Appl	c 955	12.6	63.0	2857	4	US-09-270-767-10915	Sequence 10915, A
883	12.6	63.0	1335	4	US-09-328-352-3956	Sequence 3956, Ap	c 956	12.6	63.0	2870	4	US-09-799-875-16	Sequence 16, Appl
884	12.6	63.0	1350	3	US-09-049-867-1	Sequence 1, Appl	c 957	12.6	63.0	2891	4	US-09-578-441-1	Sequence 1, Appl
885	12.6	63.0	1363	4	US-09-270-767-12095	Sequence 12095, A	c 958	12.6	63.0	2925	4	US-09-540-236-384	Sequence 384, App
886	12.6	63.0	1365	4	US-09-107-532A-1559	Sequence 1559, Ap	c 959	12.6	63.0	3021	4	US-09-710-279-4315	Sequence 4315, Ap
887	12.6	63.0	1380	4	US-09-134-000C-3234	Sequence 3234, Ap	c 960	12.6	63.0	3024	1	US-08-149-100-1	Sequence 1, Appl
888	12.6	63.0	1392	4	US-09-489-039A-6771	Sequence 6771, Ap	961	12.6	63.0	3041	4	US-09-694-777A-20	Sequence 20, Appl
889	12.6	63.0	1395	4	US-09-248-796A-2111	Sequence 2111, Ap	962	12.6	63.0	3115	4	US-09-710-279-3358	Sequence 3358, Ap
890	12.6	63.0	1401	3	US-09-134-001C-229	Sequence 229, App	963	12.6	63.0	3144	4	US-09-620-312D-1097	Sequence 1097, Ap
891	12.6	63.0	1408	4	US-09-636-215-587	Sequence 587, App	964	12.6	63.0	3204	4	US-09-710-279-3940	Sequence 3940, Ap
892	12.6	63.0	1408	4	US-09-685-166A-587	Sequence 587, App	965	12.6	63.0	3244	4	US-09-710-279-3567	Sequence 3567, Ap
893	12.6	63.0	1408	4	US-09-679-426-587	Sequence 587, App	c 966	12.6	63.0	3246	4	US-09-614-221A-228	Sequence 228, App
894	12.6	63.0	1414	4	US-09-270-767-5846	Sequence 5846, Ap	c 967	12.6	63.0	3285	4	US-09-710-279-3728	Sequence 3728, Ap
895	12.6	63.0	1448	4	US-09-976-594-371	Sequence 371, App	968	12.6	63.0	3360	1	US-08-408-093-5	Sequence 5, Appl
896	12.6	63.0	1482	4	US-09-328-352-3051	Sequence 3051, Ap	969	12.6	63.0	3360	1	US-08-408-420A-5	Sequence 5, Appl
897	12.6	63.0	1521	4	US-09-134-000C-2765	Sequence 2765, Ap	970	12.6	63.0	3360	1	US-08-714-901-5	Sequence 5, Appl
898	12.6	63.0	1538	4	US-09-976-594-339	Sequence 339, App	971	12.6	63.0	3360	3	US-08-040-741-5	Sequence 5, Appl
899	12.6	63.0	1566	3	US-09-134-001C-1453	Sequence 1453, Ap	972	12.6	63.0	3363	4	US-09-792-024-33	Sequence 33, Appl
900	12.6	63.0	1605	4	US-09-023-655-194	Sequence 194, App	c 973	12.6	63.0	3475	4	US-09-710-279-4032	Sequence 4032, Ap
901	12.6	63.0	1606	4	US-09-820-004-1	Sequence 1, Appl	c 974	12.6	63.0	3504	1	US-08-485-568A-8	Sequence 8, Appl
902	12.6	63.0	1668	4	US-09-328-352-1747	Sequence 1747, Ap	c 975	12.6	63.0	3504	1	US-08-620-717A-8	Sequence 8, Appl
903	12.6	63.0	1692	4	US-09-248-796A-5903	Sequence 5903, Ap	c 976	12.6	63.0	3504	2	US-08-590-554A-5	Sequence 5, Appl


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/ NAME: Brookes, A. Anders
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PB340P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 170:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8876 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/
US-08-961-527-170
Query Match 79.0%; Score 15.8; DB 4; Length 8876;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACATGG 20
Db 4731 GTCGCAACAGTACATGG 4713

RESULT 5
US-09-270-767-5948/c
/ Sequence 5948, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 5948
/ LENGTH: 427
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/
US-09-270-767-5948
Query Match 77.0%; Score 15.4; DB 4; Length 427;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCAACAGTACATGG 20
Db 249 CGCAACAGGACATGG 233

RESULT 6
US-09-270-767-21230/c
/ Sequence 21230, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 21230
/ LENGTH: 427
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/
US-09-270-767-21230
Query Match 77.0%; Score 15.4; DB 4; Length 427;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCAACAGTACATGG 20
Db 249 CGCAACAGGACATGG 233

RESULT 7
US-08-956-171E-16
/ Sequence 16, Application US/08956171E
/ Patent No. 6593114
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/ Gil H. Choi
/ Patrick S. Dillon
/ Craig A. Rosen
/ Steven C. Barash
/ Michael R. Fannon
/
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/
COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/
CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/956,171E
/ FILING DATE: 20-Oct-1997
/ CLASSIFICATION: <Unknown>
/
PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/
ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: PB248P1
/
TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/
INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13086 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-956-171E-16
Query Match 77.0%; Score 15.4; DB 4; Length 13086;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACTCGCAACAGTACAA 17
Db 2194 AATCGCAACAGTACAA 2210

RESULT 8
US-08-781-986A-16
/ Sequence 16, Application US/08781986A
/ Patent No. 6737248
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/
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;; PRIOR FILING DATE: 1999-11-09
;; NUMBER OF SEQ ID NOS: 4472
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 109
;; LENGTH: 1278
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-109

Query Match 76.0%; Score 15.2; DB 4; Length 1278;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20
DB 129 AGTCGCAACAGTTTAATGG 148

RESULT 13
US-09-026-001A-9/c
; Sequence 9, Application US/09026001A
; Patent No. 6413760
; GENERAL INFORMATION:
; APPLICANT: Boodhoo, Amechand
; APPLICANT: Seehra, Jasbir
; APPLICANT: Shaw, Gray
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,001A
; FILING DATE: 18-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-026-001A-9

Query Match 76.0%; Score 15.2; DB 4; Length 2335;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20
DB 2184 ATTGCAACAGTAAATGG 2165

RESULT 14
US-09-026-001A-17/c
; Sequence 17, Application US/09026001A
; Patent No. 6413760
; GENERAL INFORMATION:
; APPLICANT: Boodhoo, Amechand
; APPLICANT: Seehra, Jasbir
; APPLICANT: Shaw, Gray
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,001A
; FILING DATE: 18-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2359 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-026-001A-17

Query Match 76.0%; Score 15.2; DB 4; Length 2359;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20
DB 2208 ATTGCAACAGTAAATGG 2189

RESULT 15
US-09-710-279-3876
; Sequence 3876, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: FU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3876
; LENGTH: 3172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3876

Query Match 76.0%; Score 15.2; DB 4; Length 3172;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20
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Db 501 AGTCGCAACAGTTTAATTG 520

RESULT 16

US-09-710-279-4314
; Sequence 4314 Application US/09710279
; Patent No. 6703432
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4314
; LENGTH: 3172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-4314

Query Match 76.0%; Score 15.2; DB 4; Length 3172;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20
|||||
Db 501 AGTCGCAACAGTTTAATTG 520

RESULT 17

US-09-426-290-1
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Betglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 168575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21181)...(21403)
; NAME/KEY: CDS
; LOCATION: (95252)...(95430)
; NAME/KEY: CDS
; LOCATION: (101753)...(101996)
; NAME/KEY: CDS
; LOCATION: (110324)...(110439)
; NAME/KEY: CDS
; LOCATION: (124058)...(124278)

; NAME/KEY: CDS
; LOCATION: (127009)...(127130)
; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
US-09-426-290-1

Query Match 76.0%; Score 15.2; DB 4; Length 168575;
Best Local Similarity 85.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20
|||||
Db 114928 AGTCACAAATAGTAAATGG 114947

RESULT 18

US-08-620-605D-1
; Sequence 1, Application US/08620605D
; Patent No. 5846811
; GENERAL INFORMATION:
; APPLICANT: SHIBATANI, TAKEJI
; APPLICANT: AKATSUKA, HIROYUKI
; APPLICANT: KAWAI, ERI
; TITLE OF INVENTION: GENE PARTICIPATING IN THE MECHANISM OF
; TITLE OF INVENTION: SECRETION OF ESTERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,605D
; FILING DATE: 22-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 0020-3955
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-205-8000
; TELEFAX: (703)-205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; STRAIN: Serratia marcescens Sr41
US-08-620-605D-1

Query Match 75.0%; Score 15; DB 2; Length 4465;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCAACAGTACAAT 18
|||||
Db 4242 CGCAACAGTACAAT 4256

RESULT 19

US-09-005-232A-1
; Sequence 1, Application US/09005232A
; Patent No. 5922568

GENERAL INFORMATION:
APPLICANT: SHIBATANI, TAKEJI
APPLICANT: AKATSUKA, HIROYUKI
APPLICANT: KAWAI, ERI
TITLE OF INVENTION: GENE PARTICIPATING IN THE MECHANISM OF
TITLE OF INVENTION: SECRETION OF ESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,232A
FILING DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8000
TELEFAX: (703)-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4547 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
STRAIN: Serratia marcescens Sr41
US-09-005-232A-1

Query Match 75.0%; Score 15; DB 2; Length 4547;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCAACAGTACAAT 18
|||||
DB 4242 CGCAACAGTACAAT 4256

RESULT 20
US-08-545-528D-1
Sequence 1, Application US/08545528D
Patent No. 6537773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193PI
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 580073
TYPE: DNA
ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

Query Match 75.0%; Score 15; DB 4; Length 580073;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAACAGTACAATGG 20
|||||
DB 160781 CAACAGTACAATGG 160795

RESULT 21
US-09-134-001C-2315
Sequence 2315, Application US/09134001C
Patent No. 6360370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2315
LENGTH: 192
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2315

Query Match 74.0%; Score 14.8; DB 3; Length 192;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAATG 19
|||||
DB 31 GACGATACGTACAATG 48

RESULT 22
US-09-270-767-2529/c
Sequence 2529, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2529
LENGTH: 272
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-2529

Query Match 74.0%; Score 14.8; DB 4; Length 272;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAATG 19
|||||
DB 269 GTCGCAACAGTACAATG 252

RESULT 23
US-09-270-767-17811/c
Sequence 17811, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:


```
Db      116 GAGCATACAGTACATG 133

RESULT 28
US-09-713-273A-15/c
; Sequence 15, Application US/09713273A
; Patent No. 6620987
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; TITLE OF INVENTION: STARCH R1 PHOSPHORYLATION PROTEINS
; FILE REFERENCE: BB1158 US CIP
; CURRENT APPLICATION NUMBER: US/09/713,273A
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/081,143
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: PCT/US99/07639
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/679,933
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 4846
; TYPE: DNA
; ORGANISM: Zea mays
US-09-713-273A-15

Query Match      74.0%; Score 14.8; DB 4; Length 4846;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTGCGAAACAGTACATG 19
      |||||
Db      3414 GTGCGAAACAGTACCTG 3397

RESULT 29
US-09-270-767-30016
; Sequence 30016, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30016
; LENGTH: 656
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-30016

Query Match      72.0%; Score 14.4; DB 4; Length 656;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGTCGCAACAGTACATA 16
      |||||
Db      156 AGTCGCAAGAGTACA 171

RESULT 30
US-09-270-767-13942
; Sequence 13942, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13942
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13942

Query Match      72.0%; Score 14.4; DB 4; Length 724;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGTCGCAACAGTACA 16
      |||||
Db      156 AGTCGCAAGAGTACA 171

RESULT 31
US-09-134-000C-875
; Sequence 875, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 875
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-875

Query Match      72.0%; Score 14.4; DB 4; Length 951;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCNACAGTACATGG 20
      |||||
Db      850 GCNACAGTACATGG 865

RESULT 32
US-09-540-014-26/c
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioedoxin and
; TITLE OF INVENTION: NADP-Thioedoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1014
; TYPE: cDNA
; ORGANISM: Hordeum vulgare
US-09-540-014-26/c
```

```
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26

Query Match          72.0%; Score 14.4; DB 3; Length 998;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
Db 450 GTCGCAACAGCACAA 435

RESULT 33
US-09-897-425-36/c
; Sequence 36, Application US/09897425
; Patent No. 6750046
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase sequence
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-425-36

Query Match          72.0%; Score 14.4; DB 4; Length 1002;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
Db 453 GTCGCAACAGCACAA 438

RESULT 34
US-09-897-425-37/c
; Sequence 37, Application US/09897425
; Patent No. 6750046
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
```

```
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-425-37

Query Match          72.0%; Score 14.4; DB 4; Length 1002;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
Db 453 GTCGCAACAGCACAA 438

RESULT 35
US-09-043-302-10/c
; Sequence 10, Application US/09043302
; Patent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
; APPLICANT: SCHEUERPLUG, Ina
; APPLICANT: MAIER, Jurgen
; APPLICANT: EICKERNJAGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(1568)
US-09-043-302-10

Query Match          72.0%; Score 14.4; DB 4; Length 1744;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCAACAGTACAATG 19
Db 1603 CGCAACAGGACAATG 1588

RESULT 36
US-09-543-681A-2598
; Sequence 2598, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
```

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2598
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2598

Query Match 72.0%; Score 14.4; DB 4; Length 2001;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCAAAACAGTACATGG 20
|||||
Db 714 GCAAAACAGTACATGG 729

RESULT 37
US-09-774-528-314
; Sequence 314, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Duntui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_Fl_genes Version 2.0
; SEQ ID NO 314
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (318)..(2180)
US-09-774-528-314

Query Match 72.0%; Score 14.4; DB 4; Length 2307;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCAAAACAGTACATGG 20
|||||
Db 172 GCAAACTGTACAATGG 187

RESULT 38
US-09-043-302-1/c
; Sequence 1, Application US/09043302
; Patent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas

; APPLICANT: SCHEUERPFUG, Ina
; APPLICANT: MAIER, Jürgen
; APPLICANT: EICKENJÄGER, Sandra
; APPLICANT: SCHWAN, Thomas
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Proteins Which Impart
; TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells
; FILE REFERENCE: 0147-172P
; CURRENT APPLICATION NUMBER: US/09/043,302
; CURRENT FILING DATE: 1998-06-08
; EARLIER APPLICATION NUMBER: PCT/EP96/04092
; EARLIER FILING DATE: 1995-09-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(447)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (583)..(1542)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1585)..(3111)
US-09-043-302-1

Query Match 72.0%; Score 14.4; DB 4; Length 3287;
Best Local Similarity 93.8%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCAAAACAGTACATG 19
|||||
Db 3146 CGCAAAACAGGACAATG 3131

RESULT 39
US-09-897-425-48/c
; Sequence 48, Application US/09897425
; Patent No. 6750046
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, EILEEN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDOLIN AND THIOREDOLIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 3787
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Phaseolin
; OTHER INFORMATION: promoter-thioredoxin reductase-phaseolin
; OTHER INFORMATION: terminator
; NAME/KEY: CDS
; LOCATION: (1555)..(2553)
US-09-897-425-48

Query Match 72.0%; Score 14.4; DB 4; Length 3787;
Best Local Similarity 93.8%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
|||||
Db 2007 GTCGCAACAGTACAA 1992

RESULT 40

US-09-897-425-53/c
; Sequence 53, Application US/09897425
; Patent No. 6750046
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDIXIN AND THIOREDIXIN REDUCTASE
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 4545
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Phaseolin
; OTHER INFORMATION: promoter-thioredoxin reductase cleosin-phaseolin
; OTHER INFORMATION: terminator
; NAME/KEY: CDS
; LOCATION: (1555)..(2907)
; NAME/KEY: CDS
; LOCATION: (3148)..(3312)
US-09-897-425-53

Query Match 72.0%; Score 14.4; DB 4; Length 4545;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
|||||
Db 2007 GTCGCAACAGTACAA 1992

RESULT 41

US-09-897-425-50/c
; Sequence 50, Application US/09897425
; Patent No. 6750046
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDIXIN AND THIOREDIXIN REDUCTASE
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783

; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/659,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 4546
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Phaseolin
; OTHER INFORMATION: promoter-oleosin thioredoxin reductase-phaseolin
; OTHER INFORMATION: terminator
; NAME/KEY: CDS
; LOCATION: (1555)..(1908)
; NAME/KEY: CDS
; LOCATION: (2149)..(3312)
US-09-897-425-50

Query Match 72.0%; Score 14.4; DB 4; Length 4546;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCAACAGTACAA 17
|||||
Db 2766 GTCGCAACAGTACAA 2751

RESULT 42

US-09-000-094-45
; Sequence 45, Application US/090000094
; Patent No. 6365160
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; COX, John Cooper
; FRAZER, Ian
; MCWILLIAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONEY, Margaret Bridget
; Holland
; EDWARDS, Stirling John
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPEPTIDE CONSTRUCTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,094
; FILING DATE: 21-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 4770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-000-094-45
Query Match 72.0%; Score 14.4; DB 3; Length 4770;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GCAAAACAGTACAATGG 20
Db 487 GCAAAACAATACAATGG 502
RESULT 43
US-10-011-749-45
Sequence 45, Application US/10011749
Patent No. 6726912
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011.749
FILING DATE: 11-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000.094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 4770 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-011-749-45
Query Match 72.0%; Score 14.4; DB 4; Length 4770;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GCAAAACAGTACAATGG 20
Db 487 GCAAAACAATACAATGG 502
RESULT 44
US-09-000-004-45
Sequence 45, Application US/09000004
Patent No. 6780603
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000.004
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 4770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-000-004-45

Query Match 72.0%; Score 14.4; DB 4; Length 4770;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCAACAGTACAAATGG 20
||||| |||||
Db 487 GCAACAATAACAATGG 502

RESULT 45

US-09-521-526-2
Sequence 2, Application US/09521526
Patent No. 6290965

GENERAL INFORMATION:
APPLICANT: JANSEN, KATHRYN U.
APPLICANT: HOFMANN, KATHRYN J.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE
TITLE OF INVENTION: 6A
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ

COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,526

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,468
FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8010 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cdna

US-09-521-526-2

Query Match 72.0%; Score 14.4; DB 3; Length 8010;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCAACAGTACAAATGG 20
||||| |||||
Db 3096 GCAACAATAACAATGG 3111

RESULT 46

PCI-US95-11859-2
Sequence 2, Application PC/TUS9511859
GENERAL INFORMATION:

APPLICANT: JANSEN, KATHRYN U.
APPLICANT: HOFMANN, KATHRYN J.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE
TITLE OF INVENTION: 6A

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11859

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,468
FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.

REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19307 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 8010 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

PCT-US95-11859-2

Query Match

Best Local Similarity 93.8%; Score 14.4; DB 5; Length 8010;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCAACAGTACAAATGG 20
||||| |||||
Db 3096 GCAACAATAACAATGG 3111

RESULT 47

US-09-453-702B-240
Sequence 240, Application US/09453702B
Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/110,955
/ FILING DATE: 04-DEC-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.95017
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: (608) 251-9166
/ INFORMATION FOR SEQ ID NO: 240:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10236
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 240:
US-09-453-702B-240

Query Match 72.0%; Score 14.4; DB 3; Length 10236;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGCAAAACAGTACATG 19
Db 875 CGCAAAACATTACATG 890

RESULT 48
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
;
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
```

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Query Match 72.0%; Score 14.4; DB 4; Length 1830121;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCAAAACAGTACAA 17
Db 1568257 GTCGCAAAACATTACAA 1568272

RESULT 49
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
;
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 72.0%; Score 14.4; DB 4; Length 1830121;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCAAAACAGTACAA 17
Db 1568257 GTCGCAAAACATTACAA 1568272

RESULT 50
US-10-329-960-1
; Sequence 1, Application US/10329960
```

```
; Patent No. 6742927
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; Patent No. 6742927
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36551)..(36551)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36636)..(36636)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44416)..(44416)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45593)..(45593)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65313)..(65313)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (80024)..(80024)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (100091)..(100091)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (102896)..(102896)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (105121)..(105121)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (107248)..(107248)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119750)..(119750)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (121344)..(121344)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (122167)..(122167)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
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Query Match 72.0%; Score 14.4; DB 4; Length 1830121;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCCGCAACAGTACAA 17
|||||
Db 1568257 GTCCGCAACATTACAA 1568272

Search completed: December 3, 2004, 05:52:13
Job time : 112.316 secs

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OW nucleic - nucleic search, using sw model

Run on: December 3, 2004, 01:41:45 ; Search time 2536.05 Seconds
(without alignments)
287.374 Million cell updates/sec

Title: US-10-050-189a-7
Perfect score: 20
Sequence: 1 agtcgcaaacagtaaatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	339	1	A1237821 EST234383
2	17.4	87.0	395	2	BF415163 UI-R-BJ2-
3	17.4	87.0	462	4	BM383949 UI-R-DM1-
4	17.4	87.0	660	1	A1227920 EST224615
5	17.4	87.0	671	7	CK843049 UI-R-BJ2-
6	17.4	87.0	714	8	AZ188404 SP_1011_B
7	16.8	84.0	562	8	AZ436878
8	16.8	84.0	613	6	CA374398
9	16.8	84.0	657	9	CL764044 OR_BBA013
10	16.8	84.0	660	7	CO640930 USDA-FP_1
11	16.8	84.0	742	8	AZ186566 SP_1007_A
12	16.8	84.0	773	2	BF573660 60207244
13	16.8	84.0	776	8	AZ183531 SP_1001_A
14	16.8	84.0	801	9	AC466985 Mus muscu
15	16.8	84.0	811	9	CL821232 OR_Cha004
16	16.8	84.0	1008	9	CL044783 CH216-61K
17	16.8	84.0	1027	9	CL044667 CH216-61K
18	16.8	84.0	1088	2	BE779512 601464260
19	16.4	82.0	383	7	CO182638 EC23473_5
20	16.4	82.0	438	7	CO263634 EK08124_4
21	16.4	82.0	444	8	AQ525102 HS_5232_B
22	16.4	82.0	457	6	CD062819 MA1-0027U
23	16.4	82.0	475	7	R54168 y98h04.r1
24	16.4	82.0	492	7	CO183546 EC25941.5

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588	8	AQ558513	HS_2082_B
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629	7	CO180321	EC01405.5
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760	8	BH203016	SM1-44KS
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414	4	BM642595	170006590
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698	8	BH607285	BOGKF79TF
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97	1	AA767086	AA767086
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294	8	AZ191734	SP_1019_B
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303	1	AI433124	t133b08_x
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324	1	AI434292	t141a01_x
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389	1	AA154818	tt67a03_x
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433	8	AZ158449	SP_0060_B
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462	1	AA946899	oq53f08_s
470	8	BH597313	BOGFW34TR
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472	1	AI131263	qcl7a02_x
476	8	AZ148054	SP_0011_B
476	8	AZ191069	SP_1018_B
479	1	AI652195	wb20b02_x
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482	8	AZ141792	SP_0045_A
488	5	BQ819700	1030079H0

98	15.8	79.0	489	7	C0776376	JH02012A0	C0776376	171	15.8	79.0	695	9	C4743960	OR_BBA008
99	15.8	79.0	490	1	A1434064	t141e11.x	A1434064	172	15.8	79.0	697	4	B1487091	RE70601.5
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102	15.8	79.0	499	4	B1999464	131027D0	B1999464	175	15.8	79.0	700	8	BH390038	AG-ND-138
103	15.8	79.0	503	2	AW823864	uf60e08.y	AW823864	176	15.8	79.0	702	8	B2050025	in45f06
104	15.8	79.0	506	6	CA707208	wk2c.pk0	CA707208	177	15.8	79.0	703	9	BX210178	Danio rer
105	15.8	79.0	508	1	A1830158	wj94f05.x	A1830158	178	15.8	79.0	704	8	A2208607	SP_0139A
106	15.8	79.0	510	5	BY479012	BV479012	BY479012	179	15.8	79.0	706	8	BH384313	AG-ND-126
107	15.8	79.0	512	4	BG661135	332916 MA	BG661135	180	15.8	79.0	707	8	B2024780	oe140b12
108	15.8	79.0	514	6	CD289500	SFRP4691	CD289500	181	15.8	79.0	709	4	BJS76976	BJS76976
109	15.8	79.0	515	1	AA1705515	ZJ92806.s	AA1705515	182	15.8	79.0	712	8	B2049958	in45f06
110	15.8	79.0	515	8	AZ133771	SP_0005A	AZ133771	183	15.8	79.0	717	4	B1306631	NL_5_H23
111	15.8	79.0	516	8	AZ161919	SP_0071A	AZ161919	184	15.8	79.0	717	5	B2044090	60553763
112	15.8	79.0	519	5	BQ816211	1030055H0	BQ816211	185	15.8	79.0	720	1	A1765808	w147f06
113	15.8	79.0	516	8	A2166665	SP_0088B	A2166665	186	15.8	79.0	721	8	A2188930	Mus muscu
114	15.8	79.0	521	8	A2166665	SP_0014A	A2166665	187	15.8	79.0	723	9	AG405493	1147f06
115	15.8	79.0	526	8	A2156836	SP_0014A	A2156836	188	15.8	79.0	723	9	B2059970	UI-R-F51
116	15.8	79.0	527	6	CB679716	OSNPF03J	CB679716	189	15.8	79.0	741	8	CA508071	SP_1018A
117	15.8	79.0	528	1	AA137890	mq29f02.f	AA137890	190	15.8	79.0	748	8	A2190865	SP_1018A
118	15.8	79.0	529	8	AZ161645	SP_0070A	AZ161645	191	15.8	79.0	748	8	A2184330	SP_1018A
119	15.8	79.0	537	5	BQ819699	1030079H0	BQ819699	192	15.8	79.0	751	8	A2190366	SP_1018A
120	15.8	79.0	538	8	A2142304	SP_0040B	A2142304	193	15.8	79.0	759	9	CL837717	OR_CBA006
121	15.8	79.0	540	1	A1797907	wh78909.x	A1797907	194	15.8	79.0	763	5	BX107542	BX107542
122	15.8	79.0	541	4	BM194987	L0704C05	BM194987	195	15.8	79.0	767	8	A2175673	SP_1033A
123	15.8	79.0	542	5	BQ817466	1030064D0	BQ817466	196	15.8	79.0	767	8	A2198509	SP_1037B
124	15.8	79.0	546	2	AW392735	CM3-ST027	AW392735	197	15.8	79.0	771	1	A1949664	wq13d08.x
125	15.8	79.0	549	2	BP438313	7Q07905.x	BP438313	198	15.8	79.0	772	5	B0673007	NL_9_55D
126	15.8	79.0	550	8	A2023092	RPCI-23-3	A2023092	199	15.8	79.0	773	5	BJS67648	BJS67648
127	15.8	79.0	552	1	AA137867	mq29d02.f	AA137867	200	15.8	79.0	776	5	BX264298	BX264298
128	15.8	79.0	557	5	BQ601040	AGENCOURT	BQ601040	201	15.8	79.0	776	8	BH396521	AG-ND-164
129	15.8	79.0	559	4	B1996501	1031039B0	B1996501	202	15.8	79.0	776	9	AG368521	Mus muscu
130	15.8	79.0	559	8	BJS56235	BJS56235	BJS56235	203	15.8	79.0	776	9	CL824778	CL824778
131	15.8	79.0	559	8	AZ160544	SP_0067A	AZ160544	204	15.8	79.0	791	7	CA290507	CR290507
132	15.8	79.0	566	8	BH063870	RPCI-24-3	BH063870	205	15.8	79.0	793	5	BX464599	BX464599
133	15.8	79.0	567	4	BJS66185	BJS66185	BJS66185	206	15.8	79.0	799	8	A2185722	SP_1005B
134	15.8	79.0	570	8	A2149023	SP_0020B	A2149023	207	15.8	79.0	809	8	A2198118	SP_1036B
135	15.8	79.0	579	5	B1589535	AGENCOURT	B1589535	208	15.8	79.0	812	5	BM969130	BM969130
136	15.8	79.0	587	2	AW574545	UI-HF-BK0	AW574545	209	15.8	79.0	817	9	BX230004	Danio rer
137	15.8	79.0	588	5	BQ819499	1030078D0	BQ819499	210	15.8	79.0	821	8	A2190029	SP_1016A
138	15.8	79.0	591	1	AU291469	AU291469	AU291469	211	15.8	79.0	823	9	BX225887	Danio rer
139	15.8	79.0	595	4	BJS61395	BJS61395	BJS61395	212	15.8	79.0	837	8	CA196982	CA196982
140	15.8	79.0	598	8	A2642328	1M0505L16	A2642328	213	15.8	79.0	839	8	CC412793	FURIM93B
141	15.8	79.0	606	1	AA946908	OG54a06.s	AA946908	214	15.8	79.0	842	7	CA237089	CA237089
142	15.8	79.0	607	1	A1651114	w97d12.x	A1651114	215	15.8	79.0	843	8	A2201615	SP_0053A
143	15.8	79.0	607	6	CF256344	mdvnl38.g	CF256344	216	15.8	79.0	852	4	B1526051	60320570
144	15.8	79.0	618	5	BQ038958	Pgmic.pk0	BQ038958	217	15.8	79.0	852	5	B2061894	603503070
145	15.8	79.0	620	1	A1767950	w199f09.x	A1767950	218	15.8	79.0	857	8	B2102606	CH230-237
146	15.8	79.0	626	2	BB372710	BB372710	BB372710	219	15.8	79.0	859	1	AL565034	AL565034
147	15.8	79.0	627	2	AW300452	x865b03.x	AW300452	220	15.8	79.0	862	6	CA944589	UI-CF-PNO
148	15.8	79.0	628	1	A1475689	tc93e11.x	A1475689	221	15.8	79.0	866	9	AG116091	AG116091
149	15.8	79.0	629	7	CF293284	CF293284	CF293284	222	15.8	79.0	869	8	A2209655	SP_0151A
150	15.8	79.0	630	2	AW300470	x865f03.x	AW300470	223	15.8	79.0	884	7	CA172823	CA172823
151	15.8	79.0	633	5	BG614254	602639939	BG614254	224	15.8	79.0	886	8	B2076280	AGENCOURT
152	15.8	79.0	633	5	BG115125	603487853	BG115125	225	15.8	79.0	892	4	BM801061	BM801061
153	15.8	79.0	633	6	CB330955	SPST6B.S	CB330955	226	15.8	79.0	907	9	CL486760	SAIL_441
154	15.8	79.0	634	4	BU572082	BJS72082	BU572082	227	15.8	79.0	914	6	CD359468	AGENCOURT
155	15.8	79.0	635	9	CF597011	t1gr-ssg-	CF597011	228	15.8	79.0	926	8	A2210601	SP_0154A
156	15.8	79.0	643	5	BQ554745	H4030A10-	BQ554745	229	15.8	79.0	928	1	AL581875	AL581875
157	15.8	79.0	643	6	CF328268	JMT11-05-	CF328268	230	15.8	79.0	935	8	AL560509	AL560509
158	15.8	79.0	649	7	CK095992	U440BPE02	CK095992	231	15.8	79.0	945	8	A2206490	SP_0104B
159	15.8	79.0	650	8	AZ171787	SP_0120B	AZ171787	232	15.8	79.0	948	4	BG677844	BG677844
160	15.8	79.0	654	5	BU251129	603401926	BU251129	233	15.8	79.0	948	9	CNS070X0	CNS070X0
161	15.8	79.0	659	5	BU651991	1112096G1	BU651991	234	15.8	79.0	958	4	BG258215	BG258215
162	15.8	79.0	662	5	BU484590	603842361	BU484590	235	15.8	79.0	975	5	BX840033	BX840033
163	15.8	79.0	663	9	CF505054	t1gr-ssg-	CF505054	236	15.8	79.0	982	5	CL093141	ISB1-23B1
164	15.8	79.0	667	2	B8645996	7881b04.x	B8645996	237	15.8	79.0	984	5	BQ481479	PV_GEO001
165	15.8	79.0	679	5	BU675233	UI-CF-DUI	BU675233	238	15.8	79.0	987	8	A2205197	SP_0100A
166	15.8	79.0	684	7	C0646363	ILLUMIGEN	C0646363	239	15.8	79.0	1019	5	BX840161	BX840161
167	15.8	79.0	686	4	BN064457	K501067C0	BN064457	240	15.8	79.0	1032	8	A2204146	SP_0095A
168	15.8	79.0	686	9	CL753058	OR_BBA012	CL753058	241	15.8	79.0	1074	1	AL560892	AL560892
169	15.8	79.0	690	8	AO989719	RfC00349	AO989719	242	15.8	79.0	1074	1	AL580997	AL580997
170	15.8	79.0	693	8	BH403668	AG-ND-138	BH403668	243	15.8	79.0	1085	4	BG257134	BG257134

C 244	15.8	79.0	1131	2	BE561325	BE561325	601344470	C 317	15.4	77.0	731	8	BH456426	BH456426	BOGZU23TF
C 245	15.8	79.0	1131	2	BE966333	BE966333	601678986	318	15.4	77.0	745	6	CF284974	CF284974	AGENCOURT
C 246	15.8	79.0	1450	3	AK012044	AK012044	Mus muscu	319	15.4	77.0	774	9	BX243931	BX243931	Danio rer
C 247	15.8	79.0	1889	3	AK008532	AK008532	Mus muscu	320	15.4	77.0	781	7	CF480075	CF480075	POLL_63_C
C 248	15.8	79.0	2035	3	AK052824	AK052824	Mus muscu	321	15.4	77.0	782	7	CF321468	CF321468	AGENCOURT
C 249	15.8	79.0	2715	3	CR601375	CR601375	F111-eng	322	15.4	77.0	798	8	AZ138544	AZ138544	SP_0176_A
C 250	15.8	79.0	4265	3	AK083865	AK083865	Mus muscu	323	15.4	77.0	825	5	CK799885	CK799885	AGENCOURT
C 251	15.6	78.0	884	3	CN8000CR	CN8000CR	Drosophil	324	15.4	77.0	826	5	BU616989	BU616989	UI-H-PH1-
C 252	15.4	77.0	161	7	CN796511	CN796511	DK8901227	325	15.4	77.0	846	8	CC393317	CC393317	PURHOQ3TB
C 253	15.4	77.0	171	2	BE595960	BE595960	P11_50_E0	326	15.4	77.0	868	5	CG090170	CG090170	PURPD38TD
C 254	15.4	77.0	174	4	BU094372	BU094372	BJ094372	327	15.4	77.0	874	5	BX850662	BX850662	BX850662
C 255	15.4	77.0	238	5	BQ283941	BQ283941	335_Bgh_m	328	15.4	77.0	878	1	AL669773	AL669773	AGENCOURT
C 256	15.4	77.0	279	4	BG161973	BG161973	dc44a12_Y	329	15.4	77.0	880	7	CK797394	CK797394	AGENCOURT
C 257	15.4	77.0	292	7	CN801055	CN801055	ID8PQ3074	330	15.4	77.0	881	9	CC976633	CC976633	ZUAFH93TH
C 258	15.4	77.0	296	2	BB280301	BB280301	BB280301	331	15.4	77.0	889	4	BI226754	BI226754	602951817
C 259	15.4	77.0	297	7	CN875054	CN875054	010131AR	332	15.4	77.0	898	7	CK797397	CK797397	AGENCOURT
C 260	15.4	77.0	354	8	CC372404	CC372404	FURHR70TB	333	15.4	77.0	912	1	AL665997	AL665997	AGENCOURT
C 261	15.4	77.0	360	1	AV191960	AV191960	AV191960	334	15.4	77.0	945	1	AZ138479	AZ138479	SP_0159_B
C 262	15.4	77.0	362	7	CN347880	CN347880	170006000	335	15.4	77.0	972	9	CG089444	CG089444	PURPD37TB
C 263	15.4	77.0	371	4	BI028483	BI028483	IL5-MT020	336	15.4	77.0	994	8	CC240513	CC240513	CH261-27P
C 264	15.4	77.0	371	1	AV188558	AV188558	AV188558	337	15.4	77.0	1035	5	BU711308	BU711308	SJAAAKG05
C 265	15.4	77.0	373	8	BZ305035	BZ305035	XD3284_q1	338	15.4	77.0	1063	5	BU341085	BU341085	603519949
C 266	15.4	77.0	376	7	CN445371	CN445371	Mdfw2002j	339	15.4	77.0	1101	9	CNS002L1	CNS002L1	Drosophil
C 267	15.4	77.0	380	8	AZ182817	AZ182817	SP_0190_A	340	15.4	77.0	1108	9	AG088369	AG088369	Par_trogl
C 268	15.4	77.0	405	4	BI848638	BI848638	471137_NA	341	15.4	77.0	1192	4	BG764887	BG764887	602737320
C 269	15.4	77.0	406	8	AZ861214	AZ861214	2M0167L03	342	15.4	77.0	1380	8	BZ556592	BZ556592	pacs1-60
C 270	15.4	77.0	413	6	CF090878	CF090878	QHM6G11_Y	343	15.4	77.0	1806	4	BM923620	BM923620	AGENCOURT
C 271	15.4	77.0	414	2	AW220158	AW220158	EST302641	344	15.2	76.0	129	4	BI420120	BI420120	LJ_NEST53B
C 272	15.4	77.0	440	1	AI277387	AI277387	GM58e02_X	345	15.2	76.0	129	4	BF494462	BF494462	AT03070_5
C 273	15.4	77.0	473	6	CB729744	CB729744	AMGNNUC-N	346	15.2	76.0	188	8	AZ976036	AZ976036	2M0251N14
C 274	15.4	77.0	476	2	BF598099	BF598099	sv03c01_Y	347	15.2	76.0	207	2	BE433065	BE433065	CD0269_WH
C 275	15.4	77.0	478	4	BG730447	BG730447	df44g06_Y	348	15.2	76.0	230	9	EX002712	EX002712	ArabiGDS
C 276	15.4	77.0	490	5	BI1818442	BI1818442	EX118442	349	15.2	76.0	234	8	CC104101	CC104101	RSU-K34_1
C 277	15.4	77.0	499	4	BI12860	BI12860	G002Q10_O	350	15.2	76.0	242	8	AQ268544	AQ268544	CPU-171
C 278	15.4	77.0	499	9	AG231696	AG231696	Lotus_cor	351	15.2	76.0	250	9	CG594849	CG594849	OST253427
C 279	15.4	77.0	508	7	CF430677	CF430677	NIT1_3_B1	352	15.2	76.0	254	2	BE941158	BE941158	EST420737
C 280	15.4	77.0	525	2	BE680835	BE680835	df85H01_Y	353	15.2	76.0	267	7	CR461763	CR461763	CR461763
C 281	15.4	77.0	528	4	BU051381	BU051381	EU051381	354	15.2	76.0	279	2	BE941157	BE941157	EST420736
C 282	15.4	77.0	530	4	BI447863	BI447863	dah89a07_	355	15.2	76.0	283	5	QJ159490	QJ159490	WHE2203_B
C 283	15.4	77.0	548	4	BI848659	BI848659	471161_NA	356	15.2	76.0	317	2	BE554271	BE554271	BB554271
C 284	15.4	77.0	555	1	AI779048	AI779048	EST259927	357	15.2	76.0	318	2	BE725045	BE725045	BB725045
C 285	15.4	77.0	559	2	BE678265	BE678265	df85H01_X	358	15.2	76.0	321	5	BE502417	BE502417	BB502417
C 286	15.4	77.0	578	4	BJ627703	BJ627703	BJ627703	359	15.2	76.0	321	5	BP748925	BP748925	BP748925
C 287	15.4	77.0	588	5	BU577279	BU577279	Bar68a10_	360	15.2	76.0	336	2	BB497029	BB497029	BB497029
C 288	15.4	77.0	601	9	CN965920	CN965920	BOIEL55TF	361	15.2	76.0	340	1	AA957311	AA957311	UI-R-E1-f
C 289	15.4	77.0	609	5	BE629089	BE629089	EX629089	362	15.2	76.0	344	1	AI548234	AI548234	UI-R-C3-c
C 290	15.4	77.0	610	6	CA682177	CA682177	wlm24_pk0	363	15.2	76.0	349	8	BZ775354	BZ775354	ih92a09_b
C 291	15.4	77.0	623	2	AW932582	AW932582	EST358425	364	15.2	76.0	350	4	BI299895	BI299895	UI-R-CV2-
C 292	15.4	77.0	625	4	BJ096473	BJ096473	BJ096473	365	15.2	76.0	351	1	AI846439	AI846439	UI-M-AQ1-
C 293	15.4	77.0	635	4	BU035005	BU035005	EU035005	366	15.2	76.0	358	6	BY793269	BY793269	BY793269
C 294	15.4	77.0	635	4	BU035005	BU035005	EU035005	367	15.2	76.0	361	8	AQ015383	AQ015383	CIT-HSP-2
C 295	15.4	77.0	636	4	BM650245	BM650245	170006873	368	15.2	76.0	362	1	AA197666	AA197666	mlu20a12_r
C 296	15.4	77.0	644	4	BM617150	BM617150	170006871	369	15.2	76.0	369	2	BE439116	BE439116	CD0263_WH
C 297	15.4	77.0	654	7	CF519859	CF519859	AGENCOURT	370	15.2	76.0	370	9	CNS07H02	CNS07H02	Atropheles
C 298	15.4	77.0	655	4	BJ096746	BJ096746	BJ096746	371	15.2	76.0	370	9	CG421108	CG421108	ZMMBB003
C 299	15.4	77.0	659	5	BX497206	BX497206	DKFZP779E	372	15.2	76.0	372	1	AI687487	AI687487	tp96g10_x
C 300	15.4	77.0	681	7	CF807693	CF807693	reHBQ27XD	373	15.2	76.0	373	8	AQ107384	AQ107384	HS_3105_B
C 301	15.4	77.0	671	7	CK800153	CK800153	AGENCOURT	374	15.2	76.0	374	5	BY045925	BY045925	BY045925
C 302	15.4	77.0	678	6	CB591144	CB591144	AGENCOURT	375	15.2	76.0	374	8	AZ303294	AZ303294	GSSTC1234
C 303	15.4	77.0	686	1	AV699282	AV699282	AV699282	376	15.2	76.0	374	8	AZ774993	AZ774993	2M0004G20
C 304	15.4	77.0	686	9	BX206278	BX206278	Danio rer	377	15.2	76.0	377	4	BI069646	BI069646	C005P290
C 305	15.4	77.0	697	7	CR534778	CR534778	CR534778	378	15.2	76.0	390	1	AV413237	AV413237	AV413237
C 306	15.4	77.0	699	7	CR534778	CR534778	CR534778	379	15.2	76.0	391	4	BG053378	BG053378	RH122_8_B
C 307	15.4	77.0	699	5	BX842790	BX842790	BX842790	380	15.2	76.0	400	7	CO360183	CO360183	RR_ATE_SU
C 308	15.4	77.0	699	5	BM799347	BM799347	X-EST0083	381	15.2	76.0	401	8	AZ162391	AZ162391	SP_0071_B
C 309	15.4	77.0	699	5	BX616455	BX616455	EX616455	382	15.2	76.0	403	1	AI049827	AI049827	an37g01_x
C 310	15.4	77.0	695	5	BU043110	BU043110	PP_LBa001	383	15.2	76.0	409	2	AW242300	AW242300	xm96c02_x
C 311	15.4	77.0	700	2	BJ643396	BJ643396	BJ643396	384	15.2	76.0	413	1	AI410649	AI410649	EST238942
C 312	15.4	77.0	705	8	AW644270	AW644270	cm39c10_w	385	15.2	76.0	419	8	AQ151410	AQ151410	HS_2211_A
C 313	15.4	77.0	708	1	BH971301	BH971301	odg72b07_	386	15.2	76.0	423	7	CO515906	CO515906	sl3dSG91F
C 314	15.4	77.0	709	1	AL705784	AL705784	DKFZP686M	387	15.2	76.0	423	8	AZ774984	AZ774984	2M0004B20
C 315	15.4	77.0	719	9	CC494735	CC494735	CH240_330	388	15.2	76.0	426	2	AN037701	AN037701	EST279330
C 316	15.4	77.0	721	7	CF520766	CF520766	AGENCOURT	389	15.2	76.0	431	1	AA124782	AA124782	mq05902_r
			723	6	CB592130	CB592130	AGENCOURT	390	15.2	76.0					

390	15.2	76.0	432	5	BY032286	BY032286	BY032286	463	15.2	76.0	529	2	BE714980	BE714980	ma040G03.
391	15.2	76.0	433	2	BE847675	uw29809.Y	BE847675	464	15.2	76.0	530	4	BI420976	BI420976	LJNEST639
392	15.2	76.0	434	1	AI330687	f891902.Y	AI330687	465	15.2	76.0	531	7	CO240499	CO240499	WS00713.B
393	15.2	76.0	437	8	AZ140628	SP 0002.A	AZ140628	C 466	15.2	76.0	532	7	CF641675	CF641675	D42_F06_F
394	15.2	76.0	438	1	AA073864	mm97907.F	AA073864	C 467	15.2	76.0	533	2	BE951698	BE951698	UI-M-CCO-
395	15.2	76.0	442	8	AZ140633	SP 0002.A	AZ140633	C 468	15.2	76.0	535	8	AZ952739	AZ952739	M0217L09
396	15.2	76.0	443	8	AZ145295	SP 0004.B	AZ145295	C 469	15.2	76.0	535	7	CK888617	CK888617	SGP160604
397	15.2	76.0	445	1	AI212785	y3516a1.F	AI212785	C 470	15.2	76.0	535	9	CE751938	CE751938	tiGr-ges-
398	15.2	76.0	450	4	BI138981	F120F52.Y	BI138981	C 471	15.2	76.0	539	1	AL924683	AL924683	AL24883
399	15.2	76.0	456	8	BZ855588	CH240_26B	BZ855588	C 472	15.2	76.0	540	8	AO650564	AO650564	Sheared D
400	15.2	76.0	458	7	CO253574	WS00819.B	CO253574	C 473	15.2	76.0	540	9	CL734764	CL734764	OR_BBA006
401	15.2	76.0	459	8	AZ151978	SP 0046.A	AZ151978	C 474	15.2	76.0	541	9	CE098791	CE098791	tiGr-ges-
402	15.2	76.0	460	2	AA544423	MBAFCK1D0	AA544423	C 475	15.2	76.0	544	4	BI236578	BI236578	fp37a12.X
403	15.2	76.0	462	1	BF565142	UI-R-B01-	BF565142	C 476	15.2	76.0	547	4	B1236495	B1236495	RS32556.X
404	15.2	76.0	462	9	CR495821	MediCago	CR495821	C 477	15.2	76.0	547	7	CO256426	CO256426	WS0083.B2
405	15.2	76.0	463	2	CK100151	CO05229.5	CK100151	C 478	15.2	76.0	550	2	AM618858	AM618858	EST320844
406	15.2	76.0	464	2	BF716922	NGEST3a18	BF716922	C 479	15.2	76.0	551	8	AZ206040	AZ206040	SP_0106.B
407	15.2	76.0	465	8	BF565687	UI-R-B01-	BF565687	C 480	15.2	76.0	552	4	BJ081434	BJ081434	BO81434
408	15.2	76.0	465	8	AZ903471	RPCI-24-1	AZ903471	C 481	15.2	76.0	553	4	BG883312	BG883312	fp22d04.X
409	15.2	76.0	466	4	BI1131241	G117P51.Y	BI1131241	C 482	15.2	76.0	555	4	BJ477728	BJ477728	BJ477728
410	15.2	76.0	467	1	AI615995	mg63f10.Y	AI615995	C 483	15.2	76.0	556	7	CN204799	CN204799	TS-5187.G
411	15.2	76.0	467	5	BF616133	BF616133	BF616133	C 484	15.2	76.0	557	7	CO713266	CO713266	DG14-2010
412	15.2	76.0	469	5	EQ621432	TVEST004.	EQ621432	C 485	15.2	76.0	558	5	BQ295652	BQ295652	10910380
413	15.2	76.0	471	6	BF791332	879516.MA	BF791332	C 486	15.2	76.0	560	2	BF291396	BF291396	WHE2222.D
414	15.2	76.0	472	6	CB730100	AMGNNUC.U	CB730100	C 487	15.2	76.0	561	8	AZ145926	AZ145926	SP_0035.A
415	15.2	76.0	473	8	AZ154252	SP 0035.A	AZ154252	C 488	15.2	76.0	562	5	BU084902	BU084902	SnEST4b08
416	15.2	76.0	477	8	AZ155586	SP 0002.A	AZ155586	C 489	15.2	76.0	563	7	CN717688	CN717688	E0750C06-
417	15.2	76.0	480	4	BI808665	fm0h07.X	BI808665	C 490	15.2	76.0	563	8	AQ052862	AQ052862	V67E10.MT
418	15.2	76.0	480	5	EQ078131	fy84h07.Y	EQ078131	C 491	15.2	76.0	567	8	B2115870	B2115870	CH230-460
419	15.2	76.0	481	8	AZ049030	GSSBRU043	AZ049030	C 492	15.2	76.0	569	7	CN670201	CN670201	A0889H06-
420	15.2	76.0	481	8	BZ610424	WHADJ15TR	BZ610424	C 493	15.2	76.0	571	4	BI898272	BI898272	479344.MA
421	15.2	76.0	482	8	BH438082	BOHKB93TR	BH438082	C 494	15.2	76.0	578	4	CG884540	CG884540	fp37a12.X
422	15.2	76.0	483	5	EX351337	EX351337	EX351337	C 495	15.2	76.0	578	6	CD290326	CD290326	StfPUS38.
423	15.2	76.0	483	6	CF038761	QCH28C06.	CF038761	C 496	15.2	76.0	579	4	BI203337	BI203337	EST521377
424	15.2	76.0	484	1	AI061900	LD34963.5	AI061900	C 497	15.2	76.0	582	1	AA626370	AA626370	zu89G07.S
425	15.2	76.0	484	2	BF40767	256777.MA	BF40767	C 498	15.2	76.0	585	4	BG374362	BG374362	UI-R-CV1-
426	15.2	76.0	484	8	CK089384	CO05229.3	CK089384	C 499	15.2	76.0	585	7	CO710678	CO710678	OB_BA001
427	15.2	76.0	486	8	CO059536	1124f03.b	CO059536	C 500	15.2	76.0	585	9	CL560240	CL560240	OB_BA001
428	15.2	76.0	488	5	BU798780	SJF2BGD10	BU798780	C 501	15.2	76.0	586	8	BZ780479	BZ780479	1113h02.b
429	15.2	76.0	488	6	CF223413	PtaJX0002	CF223413	C 502	15.2	76.0	587	4	BI325236	BI325236	baa02d12.
430	15.2	76.0	488	7	CO748254	StESTbaa6	CO748254	C 503	15.2	76.0	587	6	CB496412	CB496412	omykrbhb0
431	15.2	76.0	490	1	AA890091	al52011.S	AA890091	C 504	15.2	76.0	588	4	BI234710	BI234710	RE30458.5
432	15.2	76.0	491	6	CD968642	QAN3907.Y	CD968642	C 505	15.2	76.0	588	6	CF051320	CF051320	QCM24C06.
433	15.2	76.0	492	1	AL913122	AL913122	AL913122	C 506	15.2	76.0	588	7	CN584677	CN584677	USDA-EP.1
434	15.2	76.0	494	8	AQ155388	HS_3058.A	AQ155388	C 507	15.2	76.0	589	7	CN884338	CN884338	010815AAS
435	15.2	76.0	495	6	CF120126	MTU8DD.F1	CF120126	C 508	15.2	76.0	589	4	CB076675	CB076675	hJ43a12.9
436	15.2	76.0	497	4	BI961468	MONO1_6.A	BI961468	C 509	15.2	76.0	592	8	BZ905874	BZ905874	CH240_28E
437	15.2	76.0	499	1	AI820797	an37901.X	AI820797	C 510	15.2	76.0	593	4	BM895384	BM895384	952073H06
438	15.2	76.0	499	1	AL931049	AL931049	AL931049	C 511	15.2	76.0	598	6	CB517409	CB517409	ssalrGd50
439	15.2	76.0	501	8	AZ244991	RPCI-23-8	AZ244991	C 512	15.2	76.0	598	7	CO477587	CO477587	GQ0132.B7
440	15.2	76.0	506	5	EQ076259	f22d10.Y	EQ076259	C 513	15.2	76.0	599	2	BE489326	BE489326	WHE1076.C
441	15.2	76.0	506	8	AZ182993	SP_0191.A	AZ182993	C 514	15.2	76.0	601	1	AI109610	AI109610	GH08848-5
442	15.2	76.0	507	6	CD986771	QAN2H09.Y	CD986771	C 515	15.2	76.0	602	7	CK753292	CK753292	ecs01-10C
443	15.2	76.0	507	8	AZ163986	SP 0074.B	AZ163986	C 516	15.2	76.0	602	7	CO704477	CO704477	DG32-282C
444	15.2	76.0	508	2	BF291879	WHE2201.A	BF291879	C 517	15.2	76.0	605	2	BB630123	BB630123	BB630123
445	15.2	76.0	508	2	BF40768	256778.MA	BF40768	C 518	15.2	76.0	606	4	BM540883	BM540883	qJ65e03.b
446	15.2	76.0	509	2	BE113101	UI-R-BJ1-	BE113101	C 519	15.2	76.0	608	2	BF291489	BF291489	WHE2223.E
447	15.2	76.0	511	1	AA146266	mg63f10.F	AA146266	C 520	15.2	76.0	609	9	CL223376	CL223376	ZMMBEG051
448	15.2	76.0	511	7	CO244007	WS0036.B2	CO244007	C 521	15.2	76.0	612	4	Bu629028	Bu629028	Bu629028
449	15.2	76.0	512	2	BE212537	IPbRn0033	BE212537	C 522	15.2	76.0	614	6	CA555778	CA555778	K0202601
450	15.2	76.0	515	2	AW734249	SA87f06.Y	AW734249	C 523	15.2	76.0	614	6	CD093132	CD093132	MCL-0105T
451	15.2	76.0	516	6	CF037597	QCG9d10.Y	CF037597	C 524	15.2	76.0	614	8	CN719615	CN719615	E0788C01-
452	15.2	76.0	519	5	BE036794	dh31e05.X	BE036794	C 525	15.2	76.0	614	8	BH025709	BH025709	RPCI-24-2
453	15.2	76.0	519	5	EQ246411	TaE15012B	EQ246411	C 526	15.2	76.0	615	8	AQ485780	AQ485780	WHE1053.C
454	15.2	76.0	520	4	BU098372	BU098372	BU098372	C 527	15.2	76.0	616	5	BE488651	BE488651	603761176
455	15.2	76.0	521	5	BF160768	BF160768	BF160768	C 528	15.2	76.0	618	5	BU473693	BU473693	603761176
456	15.2	76.0	521	8	AQ136533	HS_3063.B	AQ136533	C 529	15.2	76.0	618	9	CE587892	CE587892	tiGr-ges-
457	15.2	76.0	523	5	EX526923	BX526923	EX526923	C 530	15.2	76.0	620	5	BQ782060	BQ782060	UI-R-EF0-
458	15.2	76.0	523	7	CF798570	Lr PAHCF	CF798570	C 531	15.2	76.0	620	6	CD085293	CD085293	UI-M-GW0-
459	15.2	76.0	524	8	AZ099945	RPCI-23-2	AZ099945	C 532	15.2	76.0	621	2	AW116615	AW116615	fi17904.X
460	15.2	76.0	526	1	AV640474	AV640474	AV640474	C 533	15.2	76.0	621	9	CF642900	CF642900	D57_C10.F
461	15.2	76.0	528	8	AZ246185	RPCI-23-7	AZ246185	C 534	15.2	76.0	621	9	CE141005	CE141005	tiGr-ges-
462	15.2	76.0	528	8	AQ117813	HS_3000_A	AQ117813	C 535	15.2	76.0	622	2	BF012375	BF012375	UX55d03.Y

C 536	15.2	76.0	625	7	CK805088	CK805088	SGP140896	609	15.2	76.0	710	5	BU210206	BU210206	604151192
C 537	15.2	76.0	626	6	CA257189	SCSGFL419	CA257189	610	15.2	76.0	711	9	CR186504	CR186504	Reverse s
C 538	15.2	76.0	626	6	CF106675	SCSFLZONI	CF106675	611	15.2	76.0	711	9	AG406026	Mus muscu	AG406026
C 539	15.2	76.0	626	9	CC571629	CH240_447	CC571629	612	15.2	76.0	712	6	CA502277	WH54045	C
C 540	15.2	76.0	626	9	CE355639	CE355639	CE355639	613	15.2	76.0	712	6	CD822070	BN25_0430	C
C 541	15.2	76.0	627	7	CE633826	CE633826	CE633826	614	15.2	76.0	712	7	CR844330	UI-R-B11-	C
C 542	15.2	76.0	628	1	AJ769685	AJ769685	AJ769685	615	15.2	76.0	712	9	CL808772	OR_CBA002	C
C 543	15.2	76.0	628	1	BU338122	BU338122	BU338122	616	15.2	76.0	713	6	CB962456	AGENCOURT	C
C 544	15.2	76.0	629	6	CB307086	CB307086	CB307086	617	15.2	76.0	715	5	BQ511724	EST619139	C
C 545	15.2	76.0	629	6	CG950585	CG950585	CG950585	618	15.2	76.0	715	9	CG913150	CG913150	C
C 546	15.2	76.0	630	4	BM423010	BM423010	BM423010	619	15.2	76.0	716	5	BU317069	BU317069	C
C 547	15.2	76.0	631	6	CA055667	CA055667	CA055667	620	15.2	76.0	716	5	CG187993	CG187993	C
C 548	15.2	76.0	631	9	CE421189	CE421189	CE421189	621	15.2	76.0	718	5	BQ763275	EBR002_SO	C
C 549	15.2	76.0	632	6	CA599997	CA599997	CA599997	622	15.2	76.0	718	6	CD849516	CD849516	C
C 550	15.2	76.0	632	8	BH352493	BH352493	BH352493	623	15.2	76.0	722	6	CL818368	CL818368	C
C 551	15.2	76.0	634	2	AW421025	AW421025	AW421025	624	15.2	76.0	723	4	CG091518	CG091518	C
C 552	15.2	76.0	634	2	EB667911	EB667911	EB667911	625	15.2	76.0	725	6	CD210964	CD210964	C
C 553	15.2	76.0	636	4	BG101948	BG101948	BG101948	626	15.2	76.0	727	6	CA059329	CA059329	C
C 554	15.2	76.0	636	4	CO590741	CO590741	CO590741	627	15.2	76.0	729	6	CA057152	CA057152	C
C 555	15.2	76.0	637	7	CF643051	CF643051	CF643051	628	15.2	76.0	729	6	CD849515	CD849515	C
C 556	15.2	76.0	638	7	AF643051	AF643051	AF643051	629	15.2	76.0	732	6	CA232342	CA232342	C
C 557	15.2	76.0	640	8	AZ082108	AZ082108	AZ082108	630	15.2	76.0	732	6	CA232342	CA232342	C
C 558	15.2	76.0	645	5	BU886192	BU886192	BU886192	631	15.2	76.0	733	9	CB477880	CB477880	C
C 559	15.2	76.0	648	9	CL600813	CL600813	CL600813	632	15.2	76.0	734	5	BU432849	BU432849	C
C 560	15.2	76.0	649	8	BZ933678	BZ933678	BZ933678	633	15.2	76.0	734	6	CB522778	CB522778	C
C 561	15.2	76.0	649	9	CL598440	CL598440	CL598440	634	15.2	76.0	737	7	CK718814	CK718814	C
C 562	15.2	76.0	651	1	AV373833	AV373833	AV373833	635	15.2	76.0	738	9	AG490652	AG490652	C
C 563	15.2	76.0	651	4	BM735613	BM735613	BM735613	636	15.2	76.0	738	9	CL780578	CL780578	C
C 564	15.2	76.0	651	5	BQ511725	BQ511725	BQ511725	637	15.2	76.0	739	9	CG974527	CG974527	C
C 565	15.2	76.0	653	6	CA155355	CA155355	CA155355	638	15.2	76.0	741	5	BX301331	BX301331	C
C 566	15.2	76.0	654	5	BU045195	BU045195	BU045195	639	15.2	76.0	741	7	CO197879	CO197879	C
C 567	15.2	76.0	655	5	BU610744	BU610744	BU610744	640	15.2	76.0	741	8	BZ775355	BZ775355	C
C 568	15.2	76.0	658	1	AL862452	AL862452	AL862452	641	15.2	76.0	743	7	CO807072	CO807072	C
C 569	15.2	76.0	658	1	AW344143	AW344143	AW344143	642	15.2	76.0	749	7	CO569170	CO569170	C
C 570	15.2	76.0	659	5	BW272985	BW272985	BW272985	643	15.2	76.0	750	5	BQ179468	BQ179468	C
C 571	15.2	76.0	661	6	CA172398	CA172398	CA172398	644	15.2	76.0	750	9	CG715663	CG715663	C
C 572	15.2	76.0	663	4	BJ628974	BJ628974	BJ628974	645	15.2	76.0	753	8	AZ252754	AZ252754	C
C 573	15.2	76.0	664	6	CD833593	CD833593	CD833593	646	15.2	76.0	757	9	CG903086	CG903086	C
C 574	15.2	76.0	665	5	BM944457	BM944457	BM944457	647	15.2	76.0	759	7	CO561485	CO561485	C
C 575	15.2	76.0	667	5	BU759222	BU759222	BU759222	648	15.2	76.0	759	9	CO316317	CO316317	C
C 576	15.2	76.0	667	9	CL591753	CL591753	CL591753	649	15.2	76.0	761	4	BG933954	BG933954	C
C 577	15.2	76.0	668	7	CK840545	CK840545	CK840545	650	15.2	76.0	762	6	CD445259	CD445259	C
C 578	15.2	76.0	669	5	BU051324	BU051324	BU051324	651	15.2	76.0	765	9	AG586868	AG586868	C
C 579	15.2	76.0	669	8	BZ035563	BZ035563	BZ035563	652	15.2	76.0	767	8	AQ532166	AQ532166	C
C 580	15.2	76.0	672	6	BU206148	BU206148	BU206148	653	15.2	76.0	771	9	CR308515	CR308515	C
C 581	15.2	76.0	673	9	CR141732	CR141732	CR141732	654	15.2	76.0	772	9	BX211384	BX211384	C
C 582	15.2	76.0	674	2	BB082558	BB082558	BB082558	655	15.2	76.0	773	9	CL602897	CL602897	C
C 583	15.2	76.0	678	2	BB003029	BB003029	BB003029	656	15.2	76.0	774	4	BM109016	BM109016	C
C 584	15.2	76.0	679	7	CK093375	CK093375	CK093375	657	15.2	76.0	775	5	BU107281	BU107281	C
C 585	15.2	76.0	679	8	BL6764	BL6764	BL6764	658	15.2	76.0	775	5	BU416140	BU416140	C
C 586	15.2	76.0	680	8	AZ190667	AZ190667	AZ190667	659	15.2	76.0	776	9	CG156909	CG156909	C
C 587	15.2	76.0	683	5	BQ782270	BQ782270	BQ782270	660	15.2	76.0	777	6	CA403283	CA403283	C
C 588	15.2	76.0	688	1	AL691586	AL691586	AL691586	661	15.2	76.0	778	5	BU317029	BU317029	C
C 589	15.2	76.0	688	7	CN761561	CN761561	CN761561	662	15.2	76.0	781	8	AQ414598	AQ414598	C
C 590	15.2	76.0	688	7	CG051992	CG051992	CG051992	663	15.2	76.0	784	5	BM131418	BM131418	C
C 591	15.2	76.0	693	6	CF035365	CF035365	CF035365	664	15.2	76.0	785	9	CG749063	CG749063	C
C 592	15.2	76.0	693	6	CF060049	CF060049	CF060049	665	15.2	76.0	786	7	CK990312	CK990312	C
C 593	15.2	76.0	693	6	CL742557	CL742557	CL742557	666	15.2	76.0	786	7	BN507642	BN507642	C
C 594	15.2	76.0	694	6	CD832516	CD832516	CD832516	667	15.2	76.0	786	8	BM507642	BM507642	C
C 595	15.2	76.0	699	7	CN549694	CN549694	CN549694	668	15.2	76.0	788	8	CO480112	CO480112	C
C 596	15.2	76.0	700	9	CR033789	CR033789	CR033789	669	15.2	76.0	790	6	CB317654	CB317654	C
C 597	15.2	76.0	702	7	BN559013	BN559013	BN559013	670	15.2	76.0	790	6	CF449987	CF449987	C
C 598	15.2	76.0	702	7	CN549269	CN549269	CN549269	671	15.2	76.0	790	6	CF449987	CF449987	C
C 599	15.2	76.0	702	7	CN549269	CN549269	CN549269	672	15.2	76.0	801	8	BZ794187	BZ794187	C
C 600	15.2	76.0	703	9	CG913508	CG913508	CG913508	673	15.2	76.0	801	8	CG129730	CG129730	C
C 601	15.2	76.0	704	6	CD933267	CD933267	CD933267	674	15.2	76.0	802	5	BX077719	BX077719	C
C 602	15.2	76.0	704	6	CK973363	CK973363	CK973363	675	15.2	76.0	802	7	CO197806	CO197806	C
C 603	15.2	76.0	704	7	CK973363	CK973363	CK973363	676	15.2	76.0	802	9	CA478121	CA478121	C
C 604	15.2	76.0	704	9	CE749588	CE749588	CE749588	677	15.2	76.0	806	5	BU612106	BU612106	C
C 605	15.2	76.0	705	8	BH431703	BH431703	BH431703	678	15.2	76.0	806	8	BU496540	BU496540	C
C 606	15.2	76.0	706	6	CD834971	CD834971	CD834971	679	15.2	76.0	806	8	CL545284	CL545284	C
C 607	15.2	76.0	708	9	CE742517	CE742517	CE742517	680	15.2	76.0	809	9	CG086109	CG086109	C
C 608	15.2	76.0	709	9	CE528276	CE528276	CE528276	681	15.2	76.0	810	9	CG086109	CG086109	C

C 682	15.2	76.0	811	2	BF241963	601877084	C 755	15.2	76.0	1066	9	CL114542	ISB1-60G3
C 683	15.2	76.0	811	9	CC648734	OGV088TV	C 756	15.2	76.0	1100	8	CC276713	CH861-46P
C 684	15.2	76.0	816	9	AQ860695	nbe0015F	C 757	15.2	76.0	1102	8	CC224551	CH861-46P
C 685	15.2	76.0	816	7	CO717256	DG14-45e9	C 758	15.2	76.0	1118	1	AJ537937	AJ537937
C 686	15.2	76.0	817	5	BU744433	CH1#002_B	C 759	15.2	76.0	1144	8	CC302750	CH261-59J
C 687	15.2	76.0	817	9	CG086694	PUIHB64TB	C 760	15.2	76.0	1201	9	CL082723	CH261-170
C 688	15.2	76.0	820	5	BX314299	BX314299	C 761	15.2	76.0	1203	8	CG300326	CH261-185
C 689	15.2	76.0	824	7	CR411628	CR411628	C 762	15.2	76.0	1257	5	BQ221781	AGENCOURT
C 690	15.2	76.0	826	8	BH552077	BOHQV60TF	C 763	15.2	76.0	1287	5	AG435389	Mus muscu
C 691	15.2	76.0	829	8	CC524591	CH240_373	C 764	15.2	76.0	1360	5	BQ719294	AGENCOURT
C 692	15.2	76.0	831	8	AZ205229	SP_0101_A	C 765	15.2	76.0	1431	9	AG163095	Pan trogl
C 693	15.2	76.0	841	9	CG185737	PURBW86TD	C 766	15.2	76.0	1481	8	CG189296	CH261-17J
C 694	15.2	76.0	844	6	CD434102	EL01N0318	C 767	15.2	76.0	1512	8	BX556870	pacsl-60
C 695	15.2	76.0	844	7	CO225076	WS01026_B	C 768	15.2	76.0	1581	3	AV103675	zeal may
C 696	15.2	76.0	844	9	CR221817	Forward_s	C 769	15.2	76.0	1732	3	BC071058	Xenopus 1
C 697	15.2	76.0	844	9	CU558543	OB_Ba001	C 770	15.2	76.0	1801	2	BQ71058	Xenopus 1
C 698	15.2	76.0	846	7	CO808467	AGENCOURT	C 771	15.2	76.0	2154	4	BG724182	602697521
C 699	15.2	76.0	850	7	CO812354	AGENCOURT	C 772	15.2	76.0	2325	3	AK033569	Mus muscu
C 700	15.2	76.0	854	9	CG129734	PUIHT81TD	C 773	15.2	76.0	2461	3	AK034482	Mus muscu
C 701	15.2	76.0	854	9	CG343163	OGDRO7TH	C 774	15.2	76.0	2562	3	AK030398	Mus muscu
C 702	15.2	76.0	855	7	CO403064	AGENCOURT	C 775	15.2	76.0	2594	3	AK047166	Mus muscu
C 703	15.2	76.0	855	9	CNS01WIZ	ALI170468	C 776	15.2	76.0	2865	3	AK028743	Mus muscu
C 704	15.2	76.0	856	9	CNS01VNT	ALI169346	C 777	15.2	76.0	2969	3	AK011832	Mus muscu
C 705	15.2	76.0	869	8	BZ771028	mcs62B12	C 778	15.2	76.0	3333	3	AK037047	Mus muscu
C 706	15.2	76.0	869	9	CC592967	CH240_394	C 779	15.2	76.0	4743	3	AK030870	Mus muscu
C 707	15.2	76.0	872	9	CG302923	CGWAW21TV	C 780	15.2	76.0	157	6	CD020254	XXV052H0
C 708	15.2	76.0	876	9	CG319404	CG31D78TH	C 781	15.2	76.0	167	4	BM174662	UI ad 32C
C 709	15.2	76.0	877	9	CH309122	Medicago	C 782	15.2	76.0	254	2	BF388232	UI-R-CA1-
C 710	15.2	76.0	879	8	AZ210167	SP_0155_A	C 783	15.2	76.0	304	2	AK893211	CM3-NN000
C 711	15.2	76.0	885	5	BU475073	60347021A	C 784	15.2	76.0	330	1	AJ668601	AJ668601
C 712	15.2	76.0	885	6	CA459542	AGENCOURT	C 785	15.2	76.0	331	6	CA780004	MPL384_3-
C 713	15.2	76.0	889	9	CL170939	PUIFQ90TD	C 786	15.2	76.0	334	2	BE209172	BE209172
C 714	15.2	76.0	889	9	CL284242	ZMWBB062	C 787	15.2	76.0	379	1	AA313305	EST185202
C 715	15.2	76.0	891	9	CL843525	OR_CBa007	C 788	15.2	76.0	386	6	BY649374	BY649374
C 716	15.2	76.0	899	5	BX460418	BX460418	C 789	15.2	76.0	391	1	AA403070	ZV63e10_1
C 717	15.2	76.0	899	8	AZ208703	SP_0106_B	C 790	15.2	76.0	391	4	BI448128	dag71c11
C 718	15.2	76.0	902	4	BI757842	603030436	C 791	15.2	76.0	404	5	BY604530	BY604530
C 719	15.2	76.0	903	6	CA978809	AGENCOURT	C 792	15.2	76.0	412	2	BF388236	UI-R-CA1-
C 720	15.2	76.0	904	7	N756785	ID0AA19C	C 793	15.2	76.0	428	1	AL778808	AL778808
C 721	15.2	76.0	904	8	BH134880	ENTOAA17TR	C 794	15.2	76.0	429	1	AA305555	AA305555
C 722	15.2	76.0	912	9	CL122571	ISB1-82F1	C 795	15.2	76.0	448	1	AJ665735	AJ665735
C 723	15.2	76.0	916	9	CC431059	PUEJW21TD	C 796	15.2	76.0	454	4	BM601655	BM601655
C 724	15.2	76.0	918	9	CG343178	OGDRO7TV	C 797	15.2	76.0	469	8	B88132	RPCI11-18M1
C 725	15.2	76.0	919	9	LI130499	ISB1-98E1	C 798	15.2	76.0	474	8	AQ541630	AQ541630
C 726	15.2	76.0	921	8	BH137368	ENTO164TF	C 799	15.2	76.0	501	1	AJ667490	AJ667490
C 727	15.2	76.0	932	5	BU749261	CH3#025_G	C 800	15.2	76.0	519	7	CA419076	CA419076
C 728	15.2	76.0	934	5	BX686781	BX686781	C 801	15.2	76.0	523	1	AJ684218	AJ684218
C 729	15.2	76.0	934	9	CR094818	Forward_s	C 802	15.2	76.0	537	6	CD475318	na03-15m
C 730	15.2	76.0	936	9	CG981301	ZUAGS93TV	C 803	15.2	76.0	539	2	BF394636	BF394636
C 731	15.2	76.0	936	9	CG339471	OG3BH07TH	C 804	15.2	76.0	544	7	CA419077	CA419077
C 732	15.2	76.0	940	8	AZ676455	ENTF18TR	C 805	15.2	76.0	554	7	CK438930	CK438930
C 733	15.2	76.0	941	2	BF306950	601891466	C 806	15.2	76.0	589	2	BE404692	BE404692
C 734	15.2	76.0	950	9	BX958671	Forward_s	C 807	15.2	76.0	589	8	CN909560	CN909560
C 735	15.2	76.0	951	8	AZ139300	SP_0179_B	C 808	15.2	76.0	589	8	AQ381325	AQ381325
C 736	15.2	76.0	957	9	CG669003	OGUHH41TH	C 809	15.2	76.0	590	1	AL848862	AL848862
C 737	15.2	76.0	957	9	CG078802	PUEV704TD	C 810	15.2	76.0	596	1	AL799921	AL799921
C 738	15.2	76.0	961	9	CNS06JQC	T7 end of	C 811	15.2	76.0	600	9	CG307922	Reverse s
C 739	15.2	76.0	973	9	CG078801	PUEV704TB	C 812	15.2	76.0	608	1	AL861112	AL861112
C 740	15.2	76.0	977	8	CC433902	PUHSC28TD	C 813	15.2	76.0	617	7	CK968355	CK968355
C 741	15.2	76.0	980	8	CC403432	PUHHC15TB	C 814	15.2	76.0	619	5	BX074959	BX074959
C 742	15.2	76.0	980	9	CG688570	ZMWBB007	C 815	15.2	76.0	623	9	CC45237	CC45237
C 743	15.2	76.0	986	4	BM012183	603636656	C 816	15.2	76.0	645	1	AL876957	AL876957
C 744	15.2	76.0	994	2	BE374850	601226670	C 817	15.2	76.0	647	6	CD680991	CD680991
C 745	15.2	76.0	1004	9	CG933438	ZMWBB005A	C 818	15.2	76.0	654	7	BX724167	BX724167
C 746	15.2	76.0	1004	9	CL056622	CH216-83G	C 819	15.2	76.0	654	7	CR282723	CR282723
C 747	15.2	76.0	1010	9	CNS078UT	T3 end of	C 820	15.2	76.0	657	9	CL520612	CL520612
C 748	15.2	76.0	1015	6	CD485701	CFUS2.1E1	C 821	15.2	76.0	676	2	AW962153	AW962153
C 749	15.2	76.0	1016	2	BF682959	602117380	C 822	15.2	76.0	692	9	CL549343	CL549343
C 750	15.2	76.0	1024	9	CG253127	OGYB076TV	C 823	15.2	76.0	695	9	CE592291	CE592291
C 751	15.2	76.0	1029	9	CG339485	OG3BH07TV	C 824	15.2	76.0	699	9	BX158317	BX158317
C 752	15.2	76.0	1032	6	CD105565	AGENCOURT	C 825	15.2	76.0	737	8	CC083800	CC083800
C 753	15.2	76.0	1040	4	EG477139	602524351	C 826	15.2	76.0	746	7	CC0482981	CC0482981
C 754	15.2	76.0	1040	8	BZ464870	BON1144TR	C 827	15.2	76.0	748	7	CK968750	CK968750


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986 14.8 74.0 426 5 BQ19952 UI-R-DQ1-
987 14.8 74.0 426 8 A218649 HS_2002.B
988 14.8 74.0 428 1 A1075831 OZ16c04.x
989 14.8 74.0 428 7 W81888 me94405.r1
990 14.8 74.0 431 2 AW597776 sj86a06.Y
991 14.8 74.0 432 1 A121863 A121863 zn96c09.s
992 14.8 74.0 435 5 BX630884 BX630884
993 14.8 74.0 436 6 CF046929 QCK31B07.
994 14.8 74.0 437 8 A2188568 SP_1012.B
995 14.8 74.0 438 2 AW242743 xm30e09.x
996 14.8 74.0 438 8 A2188592 SP_1012.B
997 14.8 74.0 439 6 CB750216 AWGNNUC.N
998 14.8 74.0 440 6 CD346221 Strpud36.
999 14.8 74.0 441 9 BX653840 Arabidops
1000 14.8 74.0 442 6 CA727056 wde1f.pk0

ALIGNMENTS

RESULT 1
LOCUS A1237821 339 bp mRNA linear EST 31-JAN-1999
DEFINITION EST234383 Normalized rat placenta, Bento Soares Rattus sp. cDNA
ACCESSION A1237821
VERSION A1237821.1 GI:3831327
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Bonaldo,M.P., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized ventricle at 15 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone Distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 223-300,
>(TA)nSimple repeat
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..395
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone_lib="UI-R-BJ2"
/lab_host="DHI0B (Life Technologies)"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ2
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest.eng.uiowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_TISSUE=ventricle at 15 dpc
TAG_LIB=UI-R-BJ2
TAG_SEQ=GTGTC

ORIGIN
Query Match 87.0%; Score 17.4; DB 2; Length 395;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

974 14.8 74.0 419 4 BJ232296 BJ232296 BJ232296
975 14.8 74.0 419 8 A2698040 RPTC-23-2
976 14.8 74.0 421 1 A16331549 w08a03.x
977 14.8 74.0 421 2 B3946777 UI-M-B20-
978 14.8 74.0 422 8 B123735 RPTC-24-2
979 14.8 74.0 423 4 BJ233120 BJ233120
980 14.8 74.0 424 1 AA150208 Z104c07.s
981 14.8 74.0 424 9 CG611837 OST297300
982 14.8 74.0 425 1 A1422569 T196f06.x
983 14.8 74.0 425 1 A1745840 60507A11
984 14.8 74.0 425 2 A1733935 SK85C07.Y
985 14.8 74.0 425 8 A2166852 SP_0094.A
986 14.8 74.0 426 5 BQ19952 UI-R-DQ1-
987 14.8 74.0 426 8 A218649 HS_2002.B
988 14.8 74.0 428 1 A1075831 OZ16c04.x
989 14.8 74.0 428 7 W81888 me94405.r1
990 14.8 74.0 431 2 AW597776 sj86a06.Y
991 14.8 74.0 432 1 A121863 A121863 zn96c09.s
992 14.8 74.0 435 5 BX630884 BX630884
993 14.8 74.0 436 6 CF046929 QCK31B07.
994 14.8 74.0 437 8 A2188568 SP_1012.B
995 14.8 74.0 438 2 AW242743 xm30e09.x
996 14.8 74.0 438 8 A2188592 SP_1012.B
997 14.8 74.0 439 6 CB750216 AWGNNUC.N
998 14.8 74.0 440 6 CD346221 Strpud36.
999 14.8 74.0 441 9 BX653840 Arabidops
1000 14.8 74.0 442 6 CA727056 wde1f.pk0

ALIGNMENTS

RESULT 1
LOCUS A1237821 339 bp mRNA linear EST 31-JAN-1999
DEFINITION EST234383 Normalized rat placenta, Bento Soares Rattus sp. cDNA
ACCESSION A1237821
VERSION A1237821.1 GI:3831327
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Other ESTs: TC56628
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1..339
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):204463"
/db_xref="taxon:10118"
/clone_lib="RPLDG37"
/clone="RPLDG37"
/note="Normalized rat placenta, Bento Soares"
/note="Organ: placenta; Vector: pMT3Pac; Site 1: EcoRI;
Site 2: NotI"

ORIGIN
Query Match 87.0%; Score 17.4; DB 1; Length 339;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 AGTCGCAAAACAGTACAATG 19
 |||
 Db 193 AGACGCAAAACAGTACAATG 211

RESULT 3

BM383949 462 bp mRNA linear EST 17-JAN-2002
 LOCUS
 DEFINITION UI-R-DM1-ckc-i-03-0-UI.s1 UI-R-DM1 Rattus norvegicus cDNA clone

ACCESSION BM383949 GI:18184002
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Rattus norvegicus (Norway rat)

Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

1 (bases 1 to 462)
 Boraldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to verify it as a clone from the M.B.
 normalized rat prostate library cDNA Library preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.regen.com) The following repetitive
 elements were found in this cDNA sequence: 223-300,
 >(TA)n#Simple repeat

Seq primer: M13 Forward

PolyA-Yes

FEATURES

source

Location/Qualifiers

1..462
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-DM1-ckc-i-03-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-DM1"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DM1
 library is a normalized Rat Prostate library (nRPro)
 constructed in pRT37 PAC vector according to the procedure
 described by Boraldo, Lennon & Soares (Normalization and
 Subtraction: Two Approaches to Facilitate Gene Discovery.
 Genome Research 6: 791-806, 1996) The oligonucleotide
 used to prime first strand synthesis contained the
 sequence tag CCAGG between the Not I cloning site and dt18
 stretch. The Rat prostate tissue was provided by Tom
 Freeman of the Sanger Center.
 TAG_TISSUE=rat prostate
 TAG_LIB=UI-R-DM1
 TAG_SEQ=CCAGG"

ORIGIN

Query Match 87.0%; Score 17.4; DB 4; Length 462;
 Best Local Similarity 94.7%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AGTCGCAAAACAGTACAATG 19
 |||
 Db 193 AGACGCAAAACAGTACAATG 211

RESULT 4

A1227920 660 bp mRNA linear EST 20-JAN-1999
 LOCUS
 DEFINITION EST224615 Normalized rat brain, Bento Soares Rattus sp. cDNA clone

ACCESSION A1227920
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Rattus sp.

Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

1 (bases 1 to 660)
 Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Kerlavage,A.R. and Adams,M.D.

Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat

Gene Index

Unpublished (1998)

Other ESTs: TC56628

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0208

Email: nhlee@tigr.org

Seq primer: M13-21.

Location/Qualifiers

1..660

/organism="Rattus sp."

/mol_type="mRNA"

/db_xref="ATCC (inhost):2036244"

/db_xref="taxon:10118"

/clone="RBRCN62"

/clone_lib="Normalized rat brain, Bento Soares"

/note="Organ: brain; Vector: pRT3Pac; Site_1: EcoRI;

Site_2: NotI"

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 660;

Best Local Similarity 94.7%; Pred. No. 4.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19

|||

Db 214 AGACGCAAAACAGTACAATG 232

RESULT 5

CK843049 671 bp mRNA linear EST 05-MAR-2004
 LOCUS
 DEFINITION UI-R-BJ2-bov-f-09-0-UI.s10 UI-R-BJ2 Rattus norvegicus cDNA clone

ACCESSION CK843049

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

1 (bases 1 to 671)

Boraldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

MEDLINE
PUBLISHED
COMMENT

97044477
 889548
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/rat.html>
 The following repetitive elements were found in this cDNA
 sequence: 223-300, >(TA)n#Simple_repeat (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source

1..671
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BJ2-bov-f-09-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-BJ2"
 /note="Vector: pT7D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-BJ2
 library is a subtracted library derived from the following
 tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
 atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
 dpc, AV canal at 15 dpc. For a detailed description of
 the library from which this clone was derived, please
 visit our web site at ratet.eng.uiowa.edu. The
 subtraction has been previously described in (Bonaldo,
 Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"

ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 671;
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
 |||||
 DB 193 AGACGCAACAGTACAATG 211

RESULT 6
AZ188404
LOCUS
DEFINITION

SP 1011_B2 H01 SP6E Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 genomic clone Plates1011 Col=2 Row=P, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ188404.1 GI:8371583
 GSS.
 Strongylocentrotus purpuratus
 Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinozoa; Echinacea; Echinoida;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 714)
 Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
 Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T.,
 Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H.
 and Hood, L.
 A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 20402566

REFERENCE
AUTHORS

Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
 Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T.,
 Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H.
 and Hood, L.
 A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 20402566

TITLE

Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 714;
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
 |||||
 DB 302 AGTCGCAACAGTACAATG 320

RESULT 7
AZ436878
LOCUS
DEFINITION

AZ436878.1 GI:10560891
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 562)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0224 row: 0 column: 14
 Seq primer: CACACGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 562.
 Location/Qualifiers
 1..562
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0224014"

FEATURES
 source

1..714
 Location/Qualifiers
 /organism="Strongylocentrotus purpuratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:7668"
 /clone="Plate=1011 Col=2 Row=P"
 /clone_lib="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
 DH10B"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 714;
 Best Local Similarity 94.7%; Pred. No. 4.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
 |||||
 DB 302 AGTCGCAACAGTACAATG 320

RESULT 7
AZ436878
LOCUS
DEFINITION

AZ436878.1 GI:10560891
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 562)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0224 row: 0 column: 14
 Seq primer: CACACGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 562.
 Location/Qualifiers
 1..562
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0224014"

FEATURES
 source

1..714
 Location/Qualifiers
 /organism="Strongylocentrotus purpuratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:7668"
 /clone="Plate=1011 Col=2 Row=P"
 /clone_lib="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
 DH10B"

/sex="male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 562;
 Best Local Similarity 90.0%; Pred. No. 8.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20

Db 469 AGTGCACAACTGTACAATAG 450

RESULT 8

CA374398/c

LOCUS

DEFINITION 648757 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT18K05_A_F03 5', mRNA linear EST 06-NOV-2002

CA374398

CA374398.1 GI:24690768

EST.

SOURCE

ORGANISM

Oncorhynchus mykiss (rainbow trout)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 613)

Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,

Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.

Sequence analysis of a rainbow trout cDNA library and creation of a

Gene Index

Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)

Contact: Rexroad CE

USDA, ARS, National Center for Cool and Cold Water Aquaculture

11876 Leetown Road, Kearneysville, WV 25430, USA

Tel: 304 724 8340 x2129

Fax: 304 725 0351

Email: crexroad@nccwa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified by

cross match v0.990329.

Seq primer: AGCGGATACCAATTTCACAGGA.

Location/Qualifiers

1. 613

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="1RT18K05_A_F03"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="NCCWA 1RT"

/note="Vector: PCMV SPOR76; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from brain, gill, liver,

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 613;
 Best Local Similarity 90.0%; Pred. No. 8.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20

Db 568 AGTCACAACTGTACAATGG 549

RESULT 9

CL764044

LOCUS

DEFINITION CL764044 557 bp DNA linear GSS 27-JUL-2004
 OR_BBA0134L22.f OR_BBA Oryza rufipogon genomic clone OR_BBA0134L22
 5', Genomic survey sequence.

ACCESSION CL764044

VERSION CL764044.1 GI:50721991

KEYWORDS GSS.

SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 657)

Kim, H., Yu, Y., Stum, D., Rao, K., Luo, M., Jetty, R.,

Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.

OMAP Project

Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: http://genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161

Sed Error: 0.00

Plate: 0134

row: L

column: 22

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1. 657

/organism="Oryza rufipogon"

/mol_type="genomic DNA"

/db_xref="taxon:4529"

/clone="OR_BBA0134L22"

/tissue_type="young leaves"

/lab_host="DH10B-T1 phage resistant"

/clone_lib="OR_BBA"

/note="Vector: pAGIBAC1; Site 1: HindIII; Site 2: HindIII"

Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acamerone@caltech.edu
Plate: 1007 row: 1 column: 23
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 742.

FEATURES
source
1..742
Location/Qualifiers
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="Plate=1007 Col=23 Row=1"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BAC63.6; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 84.0%; Score 16.8; DB 8; Length 742;
Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGTCGCAACAGTACAATGG 20
|||||
DB 89 AGTCGCAACAGTACAATGG 70
|||||

RESULT 12
BF573660 773 bp mRNA linear EST 12-DEC-2000
602077244F2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251707 5',
mRNA sequence.
BF573660
BF573660.1 GI:11647372
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 773)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs@email.nih.gov
Tissue Procurement: ATCC/DCID/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM075 row: h column: 12
High quality sequence stop: 692.

FEATURES
source
1..773
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4251707"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 62"
/note="Organ: skin; Vector: pDNR-LTB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGGCGGCGGCACATG-3' (30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies

FEATURES
source
1..660
Location/Qualifiers
/organism="Homalodisca coagulata"
/mol_type="mRNA"
/db_xref="taxon:197043"
/clone="WHHC056 E12"
/sex="Mixed population"
/tissue_type="Adult whole body"
/dev_stage="Adult"
/lab_host="XLI-Blue"
/clone_lib="Adult Glassy-winged Sharpshooter"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 200 contiguous
bases at Trace Tuner score of 20 or better. Construction
by L Hunnicutt and PM DANG USDA,ARS, U.S. Horticultural
Res. Lab, Ft. Pierce, FL, USA."

ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 660;
Best Local Similarity 90.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGTCGCAACAGTACAATGG 20
|||||
DB 165 AATCCCAACAGTACAATGG 184
|||||

RESULT 11
AZ186566/c 742 bp DNA linear GSS 30-AUG-2000
SP_1007_A1_E12_SP6 Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plates=1007 Col=23 Row=1, genomic survey sequence.
AZ186566
AZ186566.1 GI:8369744
GSS.
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinozoa; Echinoidae; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 742)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Pousck,A.J., Livingston,B.I.,
Wray,G.A., Etensohn,C.A., Lehrsch,H., Britten,R.J., Davidson,E.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
10920195
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology

FEATURES
source
1..660
Location/Qualifiers
/organism="Homalodisca coagulata"
/mol_type="mRNA"
/db_xref="taxon:197043"
/clone="WHHC056 E12"
/sex="Mixed population"
/tissue_type="Adult whole body"
/dev_stage="Adult"
/lab_host="XLI-Blue"
/clone_lib="Adult Glassy-winged Sharpshooter"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 200 contiguous
bases at Trace Tuner score of 20 or better. Construction
by L Hunnicutt and PM DANG USDA,ARS, U.S. Horticultural
Res. Lab, Ft. Pierce, FL, USA."

ORIGIN
Query Match 84.0%; Score 16.8; DB 7; Length 660;
Best Local Similarity 90.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGTCGCAACAGTACAATGG 20
|||||
DB 165 AATCCCAACAGTACAATGG 184
|||||

RESULT 11
AZ186566/c 742 bp DNA linear GSS 30-AUG-2000
SP_1007_A1_E12_SP6 Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plates=1007 Col=23 Row=1, genomic survey sequence.
AZ186566
AZ186566.1 GI:8369744
GSS.
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinozoa; Echinoidae; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 742)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swartzell,S., Wallace,J.C., Pousck,A.J., Livingston,B.I.,
Wray,G.A., Etensohn,C.A., Lehrsch,H., Britten,R.J., Davidson,E.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
10920195
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 773;
Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20

Db 592 AGTCACCAACAGTACAATGG 611

RESULT 13

AZ183531

LOCUS

DEFINITION SP 1001 A1 B10 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1001 Col=19 Row=C, genomic survey sequence.

ACCESSION

VERSION AZ183531

KEYWORDS

SOURCE GSS.

ORGANISM

Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentroidae; Strongylocentrotus.

REFERENCE

AUTHORS

Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pouetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.

A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

MEDLINE

20402566

PubMed

10920195

COMMENT

Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1001 row: C column: 19
Seq primer: SP6
Clas: BAC ends
High quality sequence stop: 776.

FEATURES

source

1..776

/organism="Strongylocentrotus purpuratus"

/mol_type="genomic DNA"

/db_xref="taxon:7668"

/clone="Plate1001 Col=19 Row=C"

/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 776;
Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20

Db 195 AGTCGCAACAGTACAACGG 214

RESULT 14

AG466985/c

LOCUS

AG466985 801 bp DNA linear GSS 04-JUN-2004

DEFINITION

Mus musculus molossinus DNA, clone:MSMG01-356P13.T7, genomic survey sequence.

ACCESSION

AG466985

VERSION

AG466985.1

KEYWORDS

GSS.

SOURCE

Mus musculus molossinus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

TITLE

BAC end Sequences of Library MSMG01

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 801)

AUTHORS

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

TITLE

Direct Submission

JOURNAL

Submitted (17-NOV-2003)

Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan

1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMG01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center

The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyada, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..801

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMG01-356P13.T7"

/sex="male"

/tissue type="mixture of kidney and spleen"

/clone_lib="MSMG01 Mouse Male BAC Library"

Query Match 84.0%; Score 16.8; DB 9; Length 801;

Best Local Similarity 90.0%; Pred. No. 8.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATGG 20

Db 792 AGTCGCAACAGTACTATAG 773

RESULT 15

CL821232

LOCUS

CL821232

DEFINITION

3'', genomic survey sequence.

ACCESSION

CL821232

VERSION

CL821232.1

GI:51066942

GSS.

Oryza rufipogon

Oryza rufipogon

Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 811)

Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,

Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and

Wing,R.

OMAP project

JOURNAL
COMMENT

Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0040 ROW: B Column: 18
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..811
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBAC040B18"
/tissue_type="young leaves"
/dev_stages="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR Cba"
/note="Vector: pGIBAC1; Site 1: HindIII; Site 2: HindIII;
drk treated 36 hrs before harvest"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 811;
Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20
DB 694 AGTAGCAACAGTACAAATG 713

RESULT 16
LOCUS

CL044783 1008 bp DNA linear GSS 31-DEC-2003
CH216-61N14_Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-61N14, genomic survey sequence.
CL044783
CL044783.1 GI:40500696
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS

1 (bases 1 to 1008)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.

TITLE
JOURNAL
COMMENT

A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 6
High quality sequence stop: 787.

FEATURES
source

Location/Qualifiers
1..1008
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:9364"
/clone="CH216-61N14"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 1008;
Best Local Similarity 90.0%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20

DB 141 AGTTGCAACATTACAAATGG 160

RESULT 17
LOCUS

CL044667 1027 bp DNA linear GSS 31-DEC-2003
CH216-61K14_Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-61K14, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL044667
CL044667.1 GI:40500580
GSS.
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS

1 (bases 1 to 1027)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.

TITLE
JOURNAL
COMMENT

A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 5
High quality sequence stop: 815.

FEATURES
source

Location/Qualifiers
1..1027
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:9364"
/clone="CH216-61K14"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 1027;
Best Local Similarity 90.0%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAAATGG 20

DB 157 AGTTGCAACATTACAAATGG 176

RESULT 18
LOCUS

BE779512 1088 bp mRNA linear EST 20-OCT-2000
601464260F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867686 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BE779512
BE779512.1 GI:10200710
EST.
Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1088)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: U1A9614 row: 9 column: 15.
Location/Qualifiers
1..1088
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3867686"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 84.0%; Score 16.8; DB 2; Length 1088;
Best Local Similarity 90.0%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AGTCGCAACAGTACAAATGG 20
Db 542 AGTCGCAACAGTACAAATGG 561

FEATURES
source
LOCUS EC23473.383 bp mRNA linear EST 18-JUN-2004
DEFINITION melanogaster cDNA clone EC23473 5, mRNA sequence.
ACCESSION CO182638
VERSION CO182638.1 GI:48955519
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 383)
Chen, F., Laguerre, M., Cheung, L.M., Chong, A., Goldschmidt, S.,
Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C.,
Orton, A., Shao, A., Platt, D. and Swimmer, C.
Exelixis FlyTag EST Project ML01 Library
Unpublished (2004)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: EC234 row: G column: 1
High quality sequence stop: 382.
Location/Qualifiers
1..383
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"

ORIGIN
Query Match 82.0%; Score 16.4; DB 7; Length 438;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TCGCAACAGTACAAATGG 20
Db 55 TCGCAACAGTACAAATGG 38

FEATURES
source
LOCUS EC23473.444 bp DNA linear GSS 11-MAY-1999
DEFINITION HS_5232_B2_D10_SP6E_RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=808 Col=20 Row=H, genomic survey sequence.
ACCESSION AQ525102
VERSION AQ525102.1 GI:4772422

ORIGIN
Query Match 82.0%; Score 16.4; DB 7; Length 383;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TCGCAACAGTACAAATGG 20
Db 8 TCGCAACAGTACAAATGG 25

FEATURES
source
LOCUS EC23473.438 bp mRNA linear EST 23-JUN-2004
DEFINITION melanogaster cDNA clone EK089124 5, mRNA sequence.
ACCESSION CO263634
VERSION CO263634.1 GI:49149219
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 438)
Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
Peterson, S. and Swimmer, C.
Exelixis FlyTag EST Project CK01 Library
Unpublished (2004)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: EK.891 row: B column: 12
High quality sequence stop: 437.
Location/Qualifiers
1..438
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone_lib="EK089124"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site 1: NotI; Site 2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."

ORIGIN
Query Match 82.0%; Score 16.4; DB 7; Length 438;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TCGCAACAGTACAAATGG 20
Db 55 TCGCAACAGTACAAATGG 38

FEATURES
source
LOCUS AQ525102
DEFINITION HS_5232_B2_D10_SP6E_RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=808 Col=20 Row=H, genomic survey sequence.
ACCESSION AQ525102
VERSION AQ525102.1 GI:4772422

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 444)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and Hood, L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 808 Row: H Column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 444.
FEATURES
source
1..444
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clones="Plate:808 Col:20 Row:H"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
ORIGIN
Query Match 82.0%; Score 16.4; DB 8; Length 444;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GTCCGAACAGTACAATG 19
||| ||||| ||||| |||||
Db 325 GTGGCAACAGTACAATG 342
RESULT 22
CD062819/c
LOCUS CD062819 457 bp mRNA linear EST 14-SEP-2003
DEFINITION MAI-0027U-A049-G03-U.G MAI-0027 Schistosoma mansoni cDNA clone
ACCESSION MAI-0027U-A049-G03.G, mRNA sequence.
VERSION CD062819
KEYWORDS EST.
SOURCE CD062819.1 GI:34613979
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Chordata; Platyhelminthes; Trematoda; Digenea; Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 457)
AUTHORS Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Ottopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, W.F., Ho, P.L., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Miyasato, P.A., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,

Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
Nat. Genet. 35 (2), 148-157 (2003)
JOURNAL 22879928
MEDLINE 12973350
PUBMED
COMMENT Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquímica
Instituto de Química - Universidade de São Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL: http://bicinfo.iq.usp.br/schisto/
Plate: MAI-0027U-A049 Row: 3 Column: G.
FEATURES
source
1..457
Location/Qualifiers
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MAI-0027U-A049-G03.G"
/sex="mixed pool"
/dev_stage="adult"
/lab_host="Mesocricetus auratus"
/clone_lib="MAI-0027"
/note="Vector: SureClone"
ORIGIN
Query Match 82.0%; Score 16.4; DB 6; Length 457;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGTCGCAACAGTACAAT 18
||||| ||||| ||||| |||||
Db 412 AGTCGCAACAGTACAAT 395
RESULT 23
R54168
LOCUS R54168 475 bp mRNA linear EST 18-MAY-1995
DEFINITION YG98h04.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:41828 5', mRNA sequence.
ACCESSION R54168
VERSION R54168.1 GI:816070
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1865
High quality sequence stops: 327 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1865 Std Error: 0.00
Seq primer: M13Kp1
High quality sequence stop: 327.
FEATURES
  source
    1..475
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:414369"
      /db_xref="taxon:9606"
      /clone="IMAGE:41828"
      /sex="female"
      /dev_stage="73 days post natal"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares infant brain INIB"
      /notes="Organ: whole brain; Vector: Lnfmid BA; Site: 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AAGTCGAAGAATTCGGCGCGCAGGAATTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lnfmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
  Query Match      82.0%; Score 16.4; DB 7; Length 475;
  Best Local Similarity 89.3%; Pred. No. 1.3e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 1 AGTCGCAACAGTACAATG 19
      |||||
  Db 430 AGTCACAAACAGTACAANG 448

RESULT 24
CO183546
LOCUS
DEFINITION
  EC25941.5prime Exelixis FlyTag ML01 pSport-Tag21 Drosophila
  melanogaster cDNA clone EC25941 5, mRNA sequence.
ACCESSION
  CO183546
VERSION
  CO183546.1 GI:48956427
KEYWORDS
  EST.
ORGANISM
  Drosophila melanogaster (fruit fly)
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 492)
  Chen, F., Lagueux, M., Cheung, L.M., Chong, A., Goldschmidt, S.,
  Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C.,
  Orton, A., Shao, A., Platt, D. and Swimmer, C.
  Exelixis FlyTag EST Project ML01 Library
  Unpublished (2004)
  Contact: Stapleton, M.
  BDCP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: EC 259 row: D column: 5
  High quality sequence stop: 475.
  Location/Qualifiers
    source
      1..492
        /organism="Drosophila melanogaster"
        /mol_type="mRNA"
        /db_xref="taxon:7227"
        /clone="EC25941"
        /dev_stage="3rd instar larva"
        /clone_lib="Exelixis FlyTag ML01 pSport-Tag21"
        /notes="Organ: fat body; Vector: pSport1-Tag21; Site 1:
NotI; Site 2: XhoI; RNA was isolated from fat body from
3rd instar larva challenged with gram+/- bacteria. cDNA
was oligodT primed."
ORIGIN
  Query Match      82.0%; Score 16.4; DB 7; Length 579;
  Best Local Similarity 94.4%; Pred. No. 1.4e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 3 TCGCAACAGTACAATGG 20
      |||||
  Db 327 TCGCCACAGTACAATGG 344

RESULT 26
AQ558513/c
LOCUS
DEFINITION
  HS.2082.B1.B09.MR.CIT.Approved.Human.Genomic.Sperm.Library.D.Homo
  sapiens_genomic clone Plate=2082 Col=17 Row=D, genomic survey
  sequence.
ACCESSION
  AQ558513
VERSION
  AQ558513.1 GI:4918245
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens

```

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ORIGIN
  Query Match      82.0%; Score 16.4; DB 7; Length 492;
  Best Local Similarity 94.4%; Pred. No. 1.4e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 3 TCGCAACAGTACAATGG 20
      |||||
  Db 382 TCGCCACAGTACAATGG 399

RESULT 25
CO192867
LOCUS
DEFINITION
  CO192867.5prime Exelixis FlyTag ML01 pSport-Tag21 Drosophila
  melanogaster cDNA clone EC34672 5, mRNA sequence.
ACCESSION
  CO192867
VERSION
  CO192867.1 GI:49004042
KEYWORDS
  EST.
ORGANISM
  Drosophila melanogaster (fruit fly)
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 579)
  Chen, F., Lagueux, M., Cheung, L.M., Chong, A., Goldschmidt, S.,
  Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C.,
  Orton, A., Shao, A., Platt, D. and Swimmer, C.
  Exelixis FlyTag EST Project ML01 Library
  Unpublished (2004)
  Contact: Stapleton, M.
  BDCP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: EC 346 row: F column: 12
  High quality sequence stop: 574.
  Location/Qualifiers
    source
      1..579
        /organism="Drosophila melanogaster"
        /mol_type="mRNA"
        /db_xref="taxon:7227"
        /clone="EC34672"
        /dev_stage="3rd instar larva"
        /clone_lib="Exelixis FlyTag ML01 pSport-Tag21"
        /notes="Organ: fat body; Vector: pSport1-Tag21; Site 1:
NotI; Site 2: XhoI; RNA was isolated from fat body from
3rd instar larva challenged with gram+/- bacteria. cDNA
was oligodT primed."
ORIGIN
  Query Match      82.0%; Score 16.4; DB 7; Length 579;
  Best Local Similarity 94.4%; Pred. No. 1.4e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  QY 3 TCGCAACAGTACAATGG 20
      |||||
  Db 327 TCGCCACAGTACAATGG 344

RESULT 26
AQ558513
LOCUS
DEFINITION
  HS.2082.B1.B09.MR.CIT.Approved.Human.Genomic.Sperm.Library.D.Homo
  sapiens_genomic clone Plate=2082 Col=17 Row=D, genomic survey
  sequence.
ACCESSION
  AQ558513
VERSION
  AQ558513.1 GI:4918245
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 588)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2082 row: D column: 17
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 588.

Location/Qualifiers
1..588

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=2082 Col=17 Row=D"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: Sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 82.0%; Score 16.4; DB 8; Length 588;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1 AGTCGCAACAGTACAAT 18

|||||

490 AGTCGCAACAGGACAAT 473

Db

RESULT 27

CK806306

LOCUS

DEFINITION

AGENCOURT 19146459 NICHG XGC Te2 Xenopus laevis cDNA clone

IMAGE:7209189 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..614

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:7209189"

/tissue_type="pooled samples from 6 adult Xenopus testis"

/lab host="DH10B Tona"

/clone_lib="NICHG XGC Te2"

/note="Organ: testis; Vector: pExpress-1; Site 1: EcorV; Site 2: NotI; RNA obtained from 6 adult male testis. CDNA was primed using oligo-dt primer: 5'-pGACTAGTTAGTCGCGCCGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.25 kb. This is a primary library (normalized primary library is NICHG XGC Te2N) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"

ORIGIN

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

<http://image.llnl.gov>

Plate: L1AM15096 row: d column: 19

High quality sequence stop: 615.

Location/Qualifiers

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/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:7209189"

/tissue_type="pooled samples from 6 adult Xenopus testis"

/lab host="DH10B Tona"

/clone_lib="NICHG XGC Te2"

/note="Organ: testis; Vector: pExpress-1; Site 1: EcorV; Site 2: NotI; RNA obtained from 6 adult male testis. CDNA was primed using oligo-dt primer: 5'-pGACTAGTTAGTCGCGCCGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.25 kb. This is a primary library (normalized primary library is NICHG XGC Te2N) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"

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Query Match 82.0%; Score 16.4; DB 7; Length 614;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCGCAACAGTACAATGG 20

|||||

Db 159 TCACAAACAGTACAATGG 176

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FEATURES

source

1..614

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:7209189"

/tissue_type="pooled samples from 6 adult Xenopus testis"

/lab host="DH10B Tona"

/clone_lib="NICHG XGC Te2"

/note="Organ: testis; Vector: pExpress-1; Site 1: EcorV; Site 2: NotI; RNA obtained from 6 adult male testis. CDNA was primed using oligo-dt primer: 5'-pGACTAGTTAGTCGCGCCGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.25 kb. This is a primary library (normalized primary library is NICHG XGC Te2N) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library"

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(Frederick, MD). Note: this is a NIH_MGC library"

Query Match	82.0%;	Score 16.4;	DB 7;	Length 629;
Best Local Similarity	94.4%;	Pred. No. 1.4e+03;		
Matches	17;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
<hr/>				
QY	3	TCGCAAAACAGTACAATGG	20	
Db	188	TCGCAACAGTACAATGG	205	
<hr/>				
RESULT 29			715 bp	linear
CA789508			715 bp	linear
LOCUS				EST 04-DEC-2002
DEFINITION				AGENCOURT 10317412 NICHDXGC 001 Xenopus laevis cDNA clone
				IMAGE:50852235 5', mRNA sequence.
ACCESSION				CA789508
VERSION				CA789508.1 GI:26034631
KEYWORDS				EST.
SOURCE				Xenopus laevis (African clawed frog)
ORGANISM				Xenopus laevis
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
				Xenopodinae; Xenopus; Xenopus.
REFERENCE				1 (bases 1 to 715)
AUTHORS				NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE				National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL				Tumor Gene Index
COMMENT				Unpublished (1997)
				Contact: Robert Strausberg, Ph.D.
				Email: craps-remail.nih.gov
				Tissue Procurement: Martha Rabbert, Steven L. Klein, Ph.D.
				CDNA Library Preparation: Life Technologies, Inc.
				CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
				DNA sequencing by: Agencourt Bioscience Corporation
				Clone distribution: MCI-CGAP clone distribution information can be
				found through the I.M.A.G.E. Consortium/LLNL at:
				http://image.llnl.gov
				Plate: LLAM11228 row: b column: 20
				High quality sequence stop: 641.
FEATURES				Location/Qualifiers
source				1..715
				/organism="Xenopus laevis"
				/mol_type="mRNA"
				/db_xref="taxon:8355"
				/clone="IMAGE:5085235"
				/tissue_type="oocytes"
				/lab_host="DH10B (phage-resistant)"
				/clone_lib="NICHDXGC 001"
				/note="vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;
				Cloned unidirectionally. Primer: Oligo dt. Average insert
				size 2.2 Kb. Constructed by Life Technologies."
ORIGIN				
Query Match	82.0%;	Score 16.4;	DB 6;	Length 715;
Best Local Similarity	94.4%;	Pred. No. 1.4e+03;		
Matches	17;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
<hr/>				
QY	3	TCGCAAAACAGTACAATGG	20	
Db	154	TCACAAACAGTACAATGG	171	
<hr/>				
RESULT 30			760 bp	linear
BH203016			760 bp	linear
LOCUS				GSS 15-NOV-2002
DEFINITION				Sml-44K5.TR Sml Schistosoma mansoni genomic clone Sml-44K5, genomic
				survey sequence.
ACCESSION				BH203016
VERSION				BH203016.1 GI:16376161
KEYWORDS				GSS.
SOURCE				Schistosoma mansoni
ORGANISM				Schistosoma mansoni
				Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
				Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

```

FEATURES
  source
    Location/Qualifiers
      1..1536
        /organism="Gossypium hirsutum"
        /mol_type="mRNA"
        /cultivar="Zhongmian12"
        /db_xref="taxon:3635"
        /clone="suc08h10r3"
        /tissue_type="ovule"
        /dev_stage="first day the flower opens"
        /clone_lib="Gossypium hirsutum ovule first day the flower
        opens"

ORIGIN
  Query Match      82.0%; Score 16.4; DB 1; Length 1536;
  Best Local Similarity 94.4%; Pred. No. 1.5e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCAACAGTACAATG 19
    ||||| ||||| ||||| ||||| |||||
Db 1365 GTCGCTAACAGTACAATG 1382

RESULT 32
BM642595/c
LOCUS
DEFINITION 17000659025141 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
ACCESSION BM642595
VERSION BM642595.1 GI:18942106
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 414)
AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celaera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celaera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: Holtra@cclera.com
Plate: NU01004SR row: O column: 06
Seq primer: M13 Reverse.
Location/Qualifiers
  1..414
    /organism="Anopheles gambiae"
    /mol_type="mRNA"
    /strain="RSP-ST (Reduced susc. to Permethrin - std.
    chromosome)"
    /db_xref="taxon:7165"
    /clone="19600447012327"
    /dev_stage="Adult"
    /lab_host="DH10B"
    /clone_lib="A.Gam.ad.cDNA1"
    /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
    adult mosquitoes (mixed sex) frozen on liquid nitrogen.
    cDNA inserts >500 bp cloned directionally into pSport 1.
    Not 1 site is 3'. Clones available through the Malaria
    Research and Reference Reagent Resource Center
    (www.malaria.mr4.org)."

ORIGIN
  Query Match      80.0%; Score 16; DB 4; Length 414;
  Best Local Similarity 100.0%; Pred. No. 2.2e+03;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTCGCAACAGTACAA 17
    ||||| ||||| ||||| ||||| |||||

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Db 337 GTCGCAACAGTACAA 322

RESULT 33
CK539992
LOCUS
DEFINITION rswb0_003251.y1 swb Bombyx mori cDNA, mRNA sequence.
ACCESSION CK539992
VERSION CK539992.1 GI:40924446
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
REFERENCE 1 (bases 1 to 603)
AUTHORS Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X.,
Cheng,T., Chai,C., Pan,G., Xu,J., Liu,C., Lin,Y., Qian,J., Hou,Y.,
Wu,Z., Li,G., Pan,M., Li,C., Shen,Y., Lan,X., Yuan,L., Yang,G.,
Wan,Y., Zhu,Y., Yu,M., Shen,W., Wu,D., Xiang,Z., Yu,J., Wang,J.,
Li,R., Li,H., Li,G., Su,J., Wang,X., Li,G., Zhang,Z., Li,J.,
Zhang,Q., Wei,N., Xu,J., Sun,H., Dong,L., Liu,D., Zhao,S., Zhao,X.,
Meng,Q., Lan,F., Fang,L., Li,Y., Wang,J., Ye,J., Wong,G.K.-S.,
Yang,H., Shi,J., Wu,Q., Li,C., Li,D., Sun,Y., Zhang,Z., Yang,Z.,
Huang,Y., Xi,Y., Qi,Q., He,D., Huang,H., Zhang,X., Wang,Z., Li,W.
and Cao,Y.
A draft sequence for the genome of the domesticated silkworm
(Bombyx mori)
JOURNAL Unpublished (2004)
COMMENT Contact: Yang Huan Ming
Beijing Genomics Institute
Chinese Academy of Sciences
Beijing Airport Industrial Zone B6, Beijing 101300, P.R.China
Email: hyang@igtp.ac.cn.
Location/Qualifiers
  1..603
    /organism="Bombyx mori"
    /mol_type="mRNA"
    /strain="BaZhao(F50)"
    /db_xref="taxon:7091"
    /sex="female"
    /tissue_type="ovary"
    /dev_stage="5th-instar day-3 larva"
    /clone_lib="swb"
    /note="Vector: pBluescript II SK(+)"

ORIGIN
  Query Match      80.0%; Score 16; DB 7; Length 603;
  Best Local Similarity 100.0%; Pred. No. 2.2e+03;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCAACAGTACAATGG 20
    ||||| ||||| ||||| ||||| |||||
Db 543 GCAACAGTACAATGG 558

RESULT 34
CK542039
LOCUS
DEFINITION rswb0_006409.y1 swb Bombyx mori cDNA, mRNA sequence.
ACCESSION CK542039
VERSION CK542039.1 GI:40926493
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
REFERENCE 1 (bases 1 to 614)
AUTHORS Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X.,
Cheng,T., Chai,C., Pan,G., Xu,J., Liu,C., Lin,Y., Qian,J., Hou,Y.,
Wu,Z., Li,G., Pan,M., Li,C., Shen,Y., Lan,X., Yuan,L., Yang,G.,
Wan,Y., Zhu,Y., Yu,M., Shen,W., Wu,D., Xiang,Z., Yu,J., Wang,J.,

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Li,R., Li,H., Li,G., Su,J., Wang,X., Li,G., Zhang,Z., Li,J.,
Zhang,Q., Wei,N., Xu,J., Sun,H., Dong,L., Liu,D., Zhao,S., Zhao,X.,
Meng,Q., Lan,F., Fang,L., Li,Y., Wang,J., Ye,J., Wong,G.K.-S.,
Yang,H., Shi,J., Wu,Q., Li,C., Li,D., Sun,Y., Zhang,Z., Yang,Z.,
Huang,Y., Xi,Y., Qi,Q., He,D., Huang,H., Zhang,X., Wang,Z., Li,W.
and Cao,Y.
A draft sequence for the genome of the domesticated silkworm
(Bombyx mori)
Unpublished (2004)
Contact: Yang Huan Ming
Beijing Genomics Institute
Chinese Academy of Sciences
Beijing Airport Industrial Zone B6, Beijing 101300, P.R.China
Email: hyan@igtp.ac.cn.
Location/Qualifiers
    source
        1. .614
            /organism="Bombyx mori"
            /mol_type="mRNA"
            /strain="DaZhao(P50)"
            /db_xref="taxon:7091"
            /sex="female"
            /tissue_type="ovary"
            /dev_stage="5th-instar day-3 larva"
            /clone_lib="gwh"
            /note="Vector: pBluescript II SK(+)"

ORIGIN
Query Match      80.0%; Score 16; DB 7; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCACACAGTACATGG 20
        |||||
Db      483 GCACACAGTACATGG 498

RESULT 35
BH459616/c
LOCUS      BH459616      616 bp      DNA      linear      GSS 13-DEC-2001
DEFINITION BOGIC86TF BOGI Brassica oleracea genomic clone BOGIC86, genomic
survey sequence.
ACCESSION      BH459616      GI:17649361
VERSION      BH459616
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 616)
AUTHORS      Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Other_GSSs: BOGIC86TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
    source
        1. .616
            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
            /strain="TO100DH3"
            /db_xref="taxon:3712"
            /clone_lib="BOGI"
            /note="Vector: pBOS1; Site 1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pBOS1 using BstXI linkers"

FEATURES
source
    CC541986
    CH240_423E19.TARAC13P2 CHORI-240 Bos taurus genomic clone
    CH240_423E19, Genomic survey sequence.
    CC541986
    GSS.
    CC541986.1 GI:31860270
    Bos taurus (cow)
    Bos taurus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
    REFERENCE      1 (bases 1 to 753)

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ORIGIN
Query Match      80.0%; Score 16; DB 8; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCAACAGTACATG 19
        |||||
Db      37 CGCAACAGTACATG 22

RESULT 36
BH607285/c
LOCUS      BH607285      698 bp      DNA      linear      GSS 15-DEC-2001
DEFINITION BOGKF79TF BOGK Brassica oleracea genomic clone BOGKF79, genomic
survey sequence.
ACCESSION      BH607285
VERSION      BH607285.1 GI:17859731
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 698)
AUTHORS      Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Other_GSSs: BOGKF79TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
    source
        1. .698
            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
            /strain="TO100DH3"
            /db_xref="taxon:3712"
            /clone_lib="BOGKF79"
            /clone_lib="BOGK"
            /note="Vector: pBOS1; Site 1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pBOS1 using BstXI linkers"

FEATURES
source
    CC541986
    CH240_423E19.TARAC13P2 CHORI-240 Bos taurus genomic clone
    CH240_423E19, Genomic survey sequence.
    CC541986
    GSS.
    CC541986.1 GI:31860270
    Bos taurus (cow)
    Bos taurus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
    REFERENCE      1 (bases 1 to 753)

```

AUTHORS

Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A. L., Teal, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown, John, M., Jones, S., Schein, J., Marra, M., de Jong, P., Keele, J. W., and Kappes, S. M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
Other GSSs: CH240 423E19..T7
Contact: Rob Holt

JOURNAL

Unpublished (2003)

COMMENT

Other GSSs: CH240 423E19..T7

Contact: Rob Holt

The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4S6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/orderinginformation.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 423 row: E column: 19
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..753
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clones="CH240_423E19"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 80.0%; Score 16; DB 9; Length 753;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCAACAGTCAATGG 20

Db 547 GCAACAGTCAATGG 532

RESULT 38

BH071204/c

LOCUS

DEFINITION BH071204 797 bp DNA linear GSS 18-JUL-2001
RPCI-24-257H19.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-257H19, genomic survey sequence.

ACCESSION BH071204

VERSION BH071204.1

KEYWORDS GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 797)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-257H19.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 257 row: H column: 19
Seq primer: SP6
Class: BAC ends.

Location/Qualifiers

1..797
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clones="RPCI-24-257H19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/notes="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI.
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male CS7BL/6J
DNA."

ORIGIN

Query Match

Best Local Similarity 80.0%; Score 16; DB 8; Length 797;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCAACAGTCAATGG 20

Db 452 GCAACAGTCAATGG 437

RESULT 39

LOCUS

DEFINITION ID0AA25DH09RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AA25DH09

5', mRNA sequence.

ACCESSION CN759587

VERSION CN759587.1

KEYWORDS GI:47533510

SOURCE EST.

ORGANISM

Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
Hunter, W., Martinez-Torres, D., Rabbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 25 row: H column: 9.

Location/Qualifiers

1..827

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

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/db_xref="taxon:7029"
/clone="ID0AAA25DH09"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="Xli-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN
Query Match 80.0%; Score 16; DB 7; Length 827;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCAACAGTACAAAT 18
|||||
Db 722 TCGCAACAGTACAAAT 707

RESULT 40
CN586897/c
LOCUS
DEFINITION
USDA-PP-129969 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum
cDNA clone WHAP091_C12, mRNA sequence.
ACCESSION
CN586897
VERSION
CN586897.1 GI:46998620
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 855)
Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.
Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)
Unpublished (2004)
Contact: Wayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL
USDA-ARS
2001 South Rock Rd., Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: whunter@ushrl.ars.usda.gov.
Location/Qualifiers
1..855
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="WHAP091_C12"
/sex="Mixed population"
/tissue_type="whole body, nymphs and adults"
/dev_stage="All"
/lab_host="Xli-Blue"
/clone_lib="Acyrthosiphon pisum, Pea Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Acyrthosiphon pisum colonies. Library by Stini
Kambhampati; Peter Dearden; David Stern, Department of
Ecology and Evolutionary Biology, Princeton University,
NJ. (609) 258-0759. A high quality EST with at least 100
contiguous bases at Trace Tumor score of 20 or better.
Sequencing of clones by Dr. PM Dang, US. Horticultural
Research Lab, Ft. Pierce, FL. (772) 462- 5940."

ORIGIN
Query Match 80.0%; Score 16; DB 7; Length 855;

```

```

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCAACAGTACAAAT 18
|||||
Db 746 TCGCAACAGTACAAAT 731

RESULT 41
AA767086
LOCUS
DEFINITION
o641h04.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1307575 3',
similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
; mRNA sequence.
ACCESSION
AA767086
VERSION
AA767086.1 GI:2819667
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 97)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1049 Std Error: 0.00
Seq primer: -40m13 fwd. E1 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..97
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1307575"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCBI"
/note="Vector: p77T3-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGAGCGCGCTCATTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 79.0%; Score 15.8; DB 1; Length 97;
Best Local Similarity 89.5%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACTCGCAACAGTACAAATG 19
|||||
Db 59 ACAGCAACAGTACAAATG 77

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RESULT 42
A1875704
DEFINITION
  uk51f07.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
  IMAGE:1972549 3', mRNA sequence.
ACCESSION
A1875704
VERSION
A1875704.1 GI:5549753
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 152)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Waller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other_ESTs: uk51f07.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:989289
Seq primer: custom primer used
High quality sequence stop: 122.
FEATURES
    source
        1..152
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL"
            /db_xref="taxon:10090"
            /clone="IMAGE:1972549"
            /sex="female"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="Sugano mouse kidney mkia"
            /note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
            (CAGCTGTGTG); Site 2: DraIII (CAGCATGTG); 1st strand cDNA
            was primed with an oligo(dT) primer
            [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
            ligated to a DraIII adaptor [TGTGGCCTACTGG], digested
            and cloned into distinct DraIII sites of the pME18S-FL3
            vector (5' site CAGCTGTGTG, 3' site CAGCATGTG). XhoI should
            be used to isolate the cDNA insert. Size selection was
            performed to exclude fragments <1.5kb. Library
            constructed by Dr. Sumio Sugano (University of Tokyo
            Institute of Medical Science). Custom primers for
            sequencing: 5' end primer CTCTGCTCTTAAAGTGTGG and 3' end
            primer CGACCTGCGCTCGAGCACA."
ORIGIN
    Query Match          79.0%; Score 15.8; DB 1; Length 152;
    Best Local Similarity 89.5%; Pred. No. 2.5e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAACAGTACAATG 19
    ||| ||||| ||||| |||||
Db 123 AGTAGCAACACACTACAATG 141

RESULT 43
AW404268/c
LOCUS
  AW404268
  DEFINITION
    UI-HF-BL0-ace-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
    194 bp mRNA linear EST 16-FEB-2000
ACCESSION
AW404268
VERSION
AW404268.1
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 241)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality

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```

IMAGE:3058467 5', mRNA sequence.
AW404268
VERSION
AW404268.1 GI:6923325
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
    Location/Qualifiers
        1..194
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3058467"
            /tissue_type="lymph"
            /cell_type="germinal center B cells"
            /cell_line="MGC85"
            /lab_host="DH10B (LTI)"
            /clone_lib="NIH_MGC 37"
            /note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN
    Query Match          79.0%; Score 15.8; DB 2; Length 194;
    Best Local Similarity 89.5%; Pred. No. 2.6e+03;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGTCGCAACAGTACAATG 19
    ||| ||||| ||||| |||||
Db 167 AGCTGCAACAGTACAATG 149

RESULT 44
A1128418
LOCUS
  A1128418
  DEFINITION
    qc67e07.x1 Soares Placenta 8to9weeks 2NbHP8to9w Homo sapiens cDNA
    clone IMAGE:1714692 3' similar to TR:002495 002495 SNB-1.; mRNA
    sequence.
ACCESSION
A1128418
VERSION
A1128418.1 GI:3596932
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 241)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality

```

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

```
1. .241
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clonelib="IMAGE:1714692"
/dev_stage="two placentae; one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clonelib="Soares placenta 8to9weeks_2NBHP8to9W"
/notes="Organ: placenta; Vector: pTV73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTCACTGGAGCGCGCGATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTV73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
```

ORIGIN

Query Match 79.0%; Score 15.8; DB 1; Length 241;
Best Local Similarity 89.5%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19

Db 2 AGTGGCAACAGCACATG 20

RESULT 45

LOCUS

DEFINITION uk30d09.x1 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE:1970513 3', mRNA sequence.

ACCESSION A1649302

VERSION A1649302.1 GI:4730136

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 241)
AUTHORS Marra,M., Haller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
COMMENT Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:987253

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Seq primer: custom primer used
High quality sequence stop: 112.
Location/Qualifiers
1. .241
/organism="Mus musculus"
/mol_type="mRNA"
/st_xref="C57BL"
/db_xref="taxon:10090"
/clonelib="IMAGE:1970513"
/sex="female"

FEATURES

Location/Qualifiers
1. .241
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clonelib="Plate=1019 Col=14 Row=N"
/clonelib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
DH10B"

ORIGIN

```
/dev_stage="adult"
/lab_host="DH10B"
/clonelib="Sugano mouse kidney mKia"
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTTACTG]; digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTCTCTTAAAGCTCGG and 3' end
primer CGACCTGCAGCTCGAGCACA."
```

ORIGIN

Query Match 79.0%; Score 15.9; DB 1; Length 241;
Best Local Similarity 89.5%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19

Db 123 AGTAGCAACACTACAATG 141

RESULT 46

LOCUS

DEFINITION

SP 1019 B2 G07 SP6E Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=1019 Col=14 Row=N, genomic survey sequence.

ACCESSION AZ191734

VERSION AZ191734.1 GI:8374913

KEYWORDS GSS.

SOURCE Strongylocentrotus purpuratus

ORGANISM Strongylocentrotus purpuratus

REFERENCE 1 (bases 1 to 294)

AUTHORS Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

MEDLINE 20402566

PUBMED 10920195

COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L

Division of Biology 156-29

California Institute of Technology

Pasadena California 91125, USA

Tel: (626) 395-8421

Fax: (626) 793-3047

Email: acameron@caltech.edu

Plate: 1019 row: N column: 14

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 294.

Location/Qualifiers

1. .294

/organism="Strongylocentrotus purpuratus"

/mol_type="genomic DNA"

/db_xref="taxon:7668"

/clonelib="Plate=1019 Col=14 Row=N"

/clonelib="Strongylocentrotus purpuratus, purple sea

urchin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli

DH10B"

```

Query Match      79.0%; Score 15.8; DB 8; Length 294;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||||| ||||||| |||||
Db 129 AGTCGCAACAGTACAACG 147

RESULT 47
AI434235
LOCUS      297 bp      mRNA      linear      EST 30-WAR-1999
DEFINITION t133b08.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2132247 3'
            similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
            ; mRNA sequence.
ACCESSION  AI434235
VERSION     AI434235.1 GI:4294759
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (Bases 1 to 297)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Life Technologies catalog #: 11547-015
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2729 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 175.
FEATURES
    source
        1..297
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2132247"
            /tissue_type="lymphoma, follicular mixed small and large
            cell"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Lym12"
            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
            Sali; Site 2: NotI; Cloned unidirectionally. Primer:
            Oligo dT. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"

ORIGIN
Query Match      79.0%; Score 15.8; DB 1; Length 297;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||||| ||||||| |||||
Db 244 AGTCGCAACAGTACAATG 262

RESULT 48
AI433124
LOCUS      303 bp      mRNA      linear      EST 13-APR-1999
DEFINITION t041902.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2120882 3'
            similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
            ; mRNA sequence.
ACCESSION  AI433124
VERSION     AI433124.1 GI:4286978
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (Bases 1 to 307)
AUTHORS   Kupfer, D.M., Drabentstot, S.D., Buchanan, K.L., Lai, H., Dyer, D.W.,
            Roe, B.A. and Murphy, J.W.
            Comparison of highly conserved intronic and exonic elements
            associated with splicing among five diverse fungal organisms
            Unpublished (2003)
            Contact: Murphy, JW
            Department of Microbiology and Immunology,
            University of Oklahoma Health Sciences Center
            Oklahoma City, OK 73190, USA
            Tel: 405-271-2133 ex2133
            Email: juneann-murphy@ouhsc.edu
            This clone is available from the Fungal Genetics Stock Center.
            Phone 913-588-7044, http://www.fgsc.net/ Contact Dr. Bruce Roe
            (broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
            Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (Bases 1 to 303)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Life Technologies catalog #: 11547-015
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1361 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 138.
FEATURES
    source
        1..303
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2120882"
            /tissue_type="lymphoma, follicular mixed small and large
            cell"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Lym12"
            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
            Sali; Site 2: NotI; Cloned unidirectionally. Primer:
            Oligo dT. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"

ORIGIN
Query Match      79.0%; Score 15.8; DB 1; Length 303;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAACAGTACAATG 19
||||| ||||||| |||||
Db 244 AGTCGCAACAGTACAATG 262

RESULT 49
CF185222/c
LOCUS      307 bp      mRNA      linear      EST 08-AUG-2003
DEFINITION h3e06j2.x1 Cryptococcus neoformans strain B3501 Cryptococcus
            neoformans var. neoformans cDNA clone h3e06j2 5', mRNA sequence.
ACCESSION  CF185222
VERSION     CF185222.1 GI:33507090
KEYWORDS   EST.
SOURCE     Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
            var. neoformans)
ORGANISM   Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
            1 (Bases 1 to 307)
            Kupfer, D.M., Drabentstot, S.D., Buchanan, K.L., Lai, H., Dyer, D.W.,
            Roe, B.A. and Murphy, J.W.
            Comparison of highly conserved intronic and exonic elements
            associated with splicing among five diverse fungal organisms
            Unpublished (2003)
            Contact: Murphy, JW
            Department of Microbiology and Immunology,
            University of Oklahoma Health Sciences Center
            Oklahoma City, OK 73190, USA
            Tel: 405-271-2133 ex2133
            Email: juneann-murphy@ouhsc.edu
            This clone is available from the Fungal Genetics Stock Center.
            Phone 913-588-7044, http://www.fgsc.net/ Contact Dr. Bruce Roe
            (broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
            Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library

```

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 AGTCGCAAAACAGTACAATG 19
|||
Db 244 AGTCGCAAAACAGTACAATG 262

Search completed: December 3, 2004, 05:48:27
Job time : 2612.05 secs

information.
Seq primer: T3
High quality sequence stop: 296.
Location/Qualifiers
1..307
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="B9501"
/db_xref="taxon:40410"
/clone="h3e06j2"
/lab_host="E. coli strain SOLR"
/clone_lib="Cryptococcus neoformans strain B3501"
/note="Vector: pBluescript SK-; Site_1: EcoRI at 5' end of cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 307;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACAATG 19
|||
Db 305 AGACGCAAAACAGTACAAG 287

RESULT 50

AI282634 324 bp mRNA linear EST 03-FEB-1999
LOCUS qv21909.x1 NCI CGAP Lym6 Homo sapiens cDNA clone IMAGE:1982272 3'
DEFINITION similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
; mRNA sequence.

ACCESSION

AI282634

VERSION

AI282634.1 GI:3920867

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 324)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Mark Raffeld, M.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1396 Std Error: 0.00
Seq primer: -400F from Gibco
High quality sequence stop: 273.
Location/Qualifiers

FEATURES

source

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/clone_lib="NCI CGAP Lym6"
/note="Organ: lymph node; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 0.8 kb. Non-amplified
library. -5' adaptor sequence: 5' GAATTCGGCAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN

Query Match 79.0%; Score 15.8; DB 1; Length 324;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2004, 20:35:25 ; Search time 285.789 Seconds
(without alignments)
367.363 Million cell updates/sec

Title: US-10-050-189A-7

Perfect score: 20
Sequence: 1 agtcgcaaacagtacaatg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : N Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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8	16.4	82.0	950	4	ABL03413
9	16.4	82.0	2901	4	ABL16514
10	16.4	82.0	3165	4	ABL03412
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13	15.8	79.0	431	10	ADF79775
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C 96 15 75.0 744 6 ABK7240
C 97 15 3449 4 AAH18518
C 98 15 4466 2 AAT39662
C 99 15 75.0 110000 2 AAT58840_1
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C 101 14.8 74.0 192 6 ABN92852
C 102 14.8 74.0 300 2 AAZ14621
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C 104 14.8 74.0 404 10 ADB50056
C 105 14.8 74.0 440 6 ABK75248
C 106 14.8 74.0 495 12 ADL11787
C 107 14.8 74.0 604 4 AAL06397
C 108 14.8 74.0 607 12 ADQ25030
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C 245	14.2	71.0	301	6	ABK76169	Abk76169 Bacillus	C 318	14.2	71.0	2121	5	AAS71559	Aas71559 DNA encod
C 246	14.2	71.0	306	10	ADG97070	Adg97070 Human col	C 319	14.2	71.0	2137	8	ACA33687	AcA33687 Prokaryot
C 247	14.2	71.0	322	8	ABX41602	Abx41602 Bovine ES	C 320	14.2	71.0	2138	4	ABL22488	AbL22488 Drosophi
C 248	14.2	71.0	328	10	ADG48234	Adg48234 Human ret	C 321	14.2	71.0	2157	6	ABQ70734	Abq70734 Listeria
C 249	14.2	71.0	338	4	AAI65415	Aai65415 Nucleotid	C 322	14.2	71.0	2233	2	AAQ66045	Aaq66045 Wnt clone
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C 260	14.2	71.0	479	4	AAI12415	Aai12415 Probe #23	C 333	14.2	71.0	3279	2	AAV84196	AAv84196 Gracilari
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C 262	14.2	71.0	479	4	AAI33770	Aai33770 Probe #24	C 335	14.2	71.0	3452	2	AAT58243	Aat58243 CHI-9a11-
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C 265	14.2	71.0	479	4	AAK37833	Aak37833 Human bon	C 338	14.2	71.0	3530	4	AZL30006	AzL30006 Drosophi
C 266	14.2	71.0	479	4	AAK02389	Aak02389 Human bra	C 339	14.2	71.0	3755	4	ABL20776	AbL20776 Drosophi
C 267	14.2	71.0	479	4	ABS27414	AbS27414 Human liv	C 340	14.2	71.0	3907	2	AAK13280	Aak13280 Enterococ
C 268	14.2	71.0	479	5	AAI02328	Aai02328 Probe #23	C 341	14.2	71.0	3907	6	ABS99075	AbS99075 Enterococ
C 269	14.2	71.0	479	6	ABS02287	AbS02287 Human gen	C 342	14.2	71.0	4013	4	ABL20778	AbL20778 Drosophi
C 270	14.2	71.0	501	10	ADH85272	Adh85272 Enterococ	C 343	14.2	71.0	4021	4	ABL15222	AbL15222 Drosophi
C 271	14.2	71.0	559	4	AAK60330	Aak60330 Human can	C 344	14.2	71.0	4235	4	AAH99661	Aah99661 Human pro
C 272	14.2	71.0	566	4	AAK92449	Aak92449 Human cdn	C 345	14.2	71.0	4235	4	ABA08948	AbA08948 Human sem
C 273	14.2	71.0	566	6	AAD30425	Aad30425 PCR prime	C 346	14.2	71.0	4235	10	ADP60162	Adp60162 Human con
C 274	14.2	71.0	566	12	ADL28876	Adl28876 3' end of	C 347	14.2	71.0	4287	10	ABL08228	AbL08228 Drosophi
C 275	14.2	71.0	588	4	AAK94029	Aak94029 Human cdn	C 348	14.2	71.0	4425	12	ADN61379	Adn61379 Photorhab
C 276	14.2	71.0	588	12	ADL30456	Adl30456 3' end of	C 349	14.2	71.0	4425	12	ADP18621	Adp18621 Photorhab
C 277	14.2	71.0	612	6	ABS51434	AbS51434 Shigella	C 350	14.2	71.0	4428	10	ACF69428	Acf69428 Photorhab
C 278	14.2	71.0	613	3	AAI16515	Aai16515 Human col	C 351	14.2	71.0	4592	8	ABZ59872	AbZ59872 Zebrafish
C 279	14.2	71.0	620	4	AAH99057	Aah99057 Human EST	C 352	14.2	71.0	4724	4	ABL04218	AbL04218 Drosophi
C 280	14.2	71.0	630	10	ABT21817	Abt21817 Breast ca	C 353	14.2	71.0	4748	10	ADG74693	Adg74693 Human kin
C 281	14.2	71.0	632	4	AAK06093	Aak06093 Human can	C 354	14.2	71.0	4773	10	ADG42031	Adg42031 Human SEM
C 282	14.2	71.0	641	6	ABQ59692	Abq59692 Human col	C 355	14.2	71.0	5292	4	ABL05905	AbL05905 Drosophi
C 283	14.2	71.0	672	10	ACF65724	AcF65724 Photorhab	C 356	14.2	71.0	5386	3	AAV10696	AAv10696 Human 3.5
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C 285	14.2	71.0	678	3	AACT9987	AacT9987 Human sec	C 358	14.2	71.0	5631	4	AAK52660	Aak52660 Human pol
C 286	14.2	71.0	702	10	ACF04664	AcF04664 Human mem	C 359	14.2	71.0	5756	4	AAK51676	Aak51676 Human pol
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C 288	14.2	71.0	753	10	ADK07801	Adk07801 Novel cod	C 361	14.2	71.0	5919	3	AAZ99317	Aaz99317 cDNA enco
C 289	14.2	71.0	765	6	ABK77621	Abk77621 Bacillus	C 362	14.2	71.0	5975	12	ADQ23189	Adq23189 Human sof
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C 292	14.2	71.0	804	8	ACA47609	Aca47609 Prokaryot	C 365	14.2	71.0	6145	3	AAZ99318	Aaz99318 Splice va
C 293	14.2	71.0	833	12	ADJ43306	Adj43306 Plant cdn	C 366	14.2	71.0	6302	4	AAK65687	Aak65687 Human imm
C 294	14.2	71.0	840	6	ABK77622	Abk77622 Bacillus	C 367	14.2	71.0	6617	12	ADL12539	AdL12539 Human ste
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C 297	14.2	71.0	950	10	ADQ09899	Adq09899 Novel DNA	C 370	14.2	71.0	10863	4	AAK46234	Aak46234 DNA encod
C 298	14.2	71.0	963	8	ACA39806	Aca39806 Prokaryot	C 371	14.2	71.0	10863	6	ABS73876	AbS73876 Human cdn
C 299	14.2	71.0	994	5	ADL62344	Adl62344 Human ova	C 372	14.2	71.0	11367	6	ABS73876	AbS73876 Human cdn
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C 303	14.2	71.0	1128	12	ADL03684	Adl03684 DNA encod	C 376	14.2	71.0	17761	4	ABK42709	AbK42709 Genomic s
C 304	14.2	71.0	1177	6	ABS65643	AbS65643 Mouse Mga	C 377	14.2	71.0	17761	4	AAK79415	Aak79415 Human imm
C 305	14.2	71.0	1219	12	ADG32159	Adg32159 DNA encod	C 378	14.2	71.0	17761	9	ADB60865	Adb60865 Connectiv
C 306	14.2	71.0	1301	12	ADG32159	Adg32159 DNA encod	C 379	14.2	71.0	21747	4	ABL09060	AbL09060 Drosophi
C 307	14.2	71.0	1428	9	ADA30293	Ada30293 DNA encod	C 380	14.2	71.0	27062	4	AAK71622	Aak71622 Human imm
C 308	14.2	71.0	1470	9	ADA29221	Ada29221 DNA encod	C 381	14.2	71.0	27062	4	AAK05346	AaK05346 Human rep
C 309	14.2	71.0	1487	2	AAK33248	Aak33248 PEBP2 alp	C 382	14.2	71.0	27062	4	ABL98215	AbL98215 Human tes
C 310	14.2	71.0	1603	4	AAK91531	Aak91531 Human dig	C 383	14.2	71.0	28874	3	AAK81505	AaK81505 N. mening
C 311	14.2	71.0	1634	6	ABZ15595	Abz15595 Arabidops	C 384	14.2	71.0	30013	4	AAK41960	AaK41960 Genomic s
C 312	14.2	71.0	1644	12	ADP04934	Adp04934 Sea squir	C 385	14.2	71.0	30013	4	AAL36932	Aal36932 Human mus
C 313	14.2	71.0	2004	5	AAS79039	Aas79039 DNA encod	C 386	14.2	71.0	30013	8	ABX59920	Abx59920 cDNA enco

C 387	14.2	71.0	30013	12	ADJ30670	Adj30670 Human mus	460	14	70.0	27150	4	ADJ30670	Adj30670 Human mus
C 388	14.2	71.0	33352	9	ADA02846	Ada02846 Human FGF	461	14	70.0	33747	4	ADA02846	Ada02846 Human FGF
C 389	14.2	71.0	33352	10	ADB72584	Adb72584 Human FGF	C 462	14	70.0	33747	4	ADB72584	Adb72584 Human FGF
C 390	14.2	71.0	33352	10	ADC85325	Adc85325 Mouse Fgf	C 463	14	70.0	110000	10	ADC85325	Adc85325 Mouse Fgf
C 391	14.2	71.0	33352	12	ADM74441	Adm74441 Human car	C 464	14	70.0	110000	12	ADM74441	Adm74441 Human car
C 392	14.2	71.0	33663	10	ADC86164	Adc86164 Human GPC	C 465	14	70.0	110000	12	ADC86164	Adc86164 Human GPC
C 393	14.2	71.0	33281	8	ADA56123	Ada56123 Human IRF	C 466	14	70.0	110000	12	ADA56123	Ada56123 Human IRF
C 394	14.2	71.0	33292	9	ADA02486	Ada02486 Human IRF	C 467	14	70.0	110000	12	ADA02486	Ada02486 Human IRF
C 395	14.2	71.0	33292	10	ADB72224	Adb72224 Human IRF	C 468	14	70.0	110000	12	ADB72224	Adb72224 Human IRF
C 396	14.2	71.0	44325	9	ADA02960	Ada02960 Human DAD	C 469	14	70.0	110000	12	ADA02960	Ada02960 Human DAD
C 397	14.2	71.0	44325	10	ADB72698	Adb72698 Human DAD	C 470	14	70.0	119211	4	ADB72698	Adb72698 Human DAD
C 398	14.2	71.0	44325	10	ADC85440	Adc85440 Human Dad	C 471	14	70.0	249878	10	ADC85440	Adc85440 Human Dad
C 399	14.2	71.0	44325	12	ADM74555	Adm74555 Human car	C 472	13.8	69.0	108	10	ADM74555	Adm74555 Human car
C 400	14.2	71.0	49431	4	ABL13742	Ab113742 Drosophil	C 473	13.8	69.0	108	10	ABL13742	Ab113742 Drosophil
C 401	14.2	71.0	59817	9	ADA02684	Ada02684 Human DUS	C 474	13.8	69.0	108	10	ADA02684	Ada02684 Human DUS
C 402	14.2	71.0	59817	10	ADB72442	Adb72442 Human DUS	C 475	13.8	69.0	114	10	ADB72442	Adb72442 Human DUS
C 403	14.2	71.0	59817	10	ADE95932	Ade95932 Human DUS	C 476	13.8	69.0	126	10	ADE95932	Ade95932 Human DUS
C 404	14.2	71.0	73947	4	ABL07230	Ab107230 Drosophil	C 477	13.8	69.0	126	10	ABL07230	Ab107230 Drosophil
C 405	14.2	71.0	81826	10	ADL13767	Adl13767 Osteoarth	C 478	13.8	69.0	144	10	ADL13767	Adl13767 Osteoarth
C 406	14.2	71.0	81826	10	ADL13783	Adl13783 Osteoarth	C 479	13.8	69.0	144	10	ADL13783	Adl13783 Osteoarth
C 407	14.2	71.0	95593	10	ADC85367	Adc85367 Mouse Blm	C 480	13.8	69.0	144	10	ADC85367	Adc85367 Mouse Blm
C 408	14.2	71.0	96594	9	ADA02888	Ada02888 Human Blm	C 481	13.8	69.0	144	10	ADA02888	Ada02888 Human Blm
C 409	14.2	71.0	96594	10	ADB72626	Adb72626 Human Blm	C 482	13.8	69.0	150	10	ADB72626	Adb72626 Human Blm
C 410	14.2	71.0	96594	10	ADC85257	Adc85257 Mouse Ptp	C 483	13.8	69.0	150	10	ADC85257	Adc85257 Mouse Ptp
C 411	14.2	71.0	96594	12	ADM74483	Adm74483 Human car	C 484	13.8	69.0	150	10	ADM74483	Adm74483 Human car
C 412	14.2	71.0	96595	9	ADA02777	Ada02777 Mouse Ptp	C 485	13.8	69.0	156	10	ADA02777	Ada02777 Mouse Ptp
C 413	14.2	71.0	96595	10	ADB72515	Adb72515 Mouse Ptp	C 486	13.8	69.0	156	10	ADB72515	Adb72515 Mouse Ptp
C 414	14.2	71.0	96595	12	ADM74372	Adm74372 Murine ca	C 487	13.8	69.0	156	10	ADM74372	Adm74372 Murine ca
C 415	14.2	71.0	96690	6	ABK12169	Abk12169 Human DNA	C 488	13.8	69.0	159	10	ABK12169	Abk12169 Human DNA
C 416	14.2	71.0	99500	6	ADA41740	Ada41740 Human REC	C 489	13.8	69.0	159	10	ADA41740	Ada41740 Human REC
C 417	14.2	71.0	110000	3	AAAB1490	Continuation (8 of	C 490	13.8	69.0	171	10	AAAB1490	Continuation (8 of
C 418	14.2	71.0	110000	6	ABQ74964	Abq74964 Human kin	C 491	13.8	69.0	171	10	ABQ74964	Abq74964 Human kin
C 419	14.2	71.0	110000	10	ACF67367	Continuation (24 o	C 492	13.8	69.0	180	10	ACF67367	Continuation (24 o
C 420	14.2	71.0	110000	10	ACF65366	Continuation (6 of	C 493	13.8	69.0	189	10	ACF65366	Continuation (6 of
C 421	14.2	71.0	159400	6	ABQ88126	Abq88126 Human ost	C 494	13.8	69.0	189	10	ABQ88126	Abq88126 Human ost
C 422	14.2	71.0	349881	10	ADC86662	Adc86662 Human GPC	C 495	13.8	69.0	192	10	ADC86662	Adc86662 Human GPC
C 423	14.2	71.0	349881	10	ADC86662	Adc86662 Human GPC	C 496	13.8	69.0	216	10	ADC86662	Adc86662 Human GPC
C 424	14.2	71.0	349880	3	AAF21608	Aaf21608 Neisseria	C 497	13.8	69.0	222	10	AAF21608	Aaf21608 Neisseria
C 425	14.2	71.0	369	12	ADL03624	Adl03624 DNA encod	C 498	13.8	69.0	230	3	ADL03624	Adl03624 DNA encod
C 426	14.2	71.0	405	12	ADL03620	Adl03620 DNA encod	C 499	13.8	69.0	247	9	ADL03620	Adl03620 DNA encod
C 427	14.2	71.0	466	4	AAI92505	Aai92505 Human pol	C 500	13.8	69.0	247	9	AAI92505	Aai92505 Human pol
C 428	14.2	71.0	479	4	ABA43569	Ab43569 Human bre	C 501	13.8	69.0	252	10	ABA43569	Ab43569 Human bre
C 429	14.2	71.0	479	4	ABA23777	Ab23777 Probe #22	C 502	13.8	69.0	270	10	ABA23777	Ab23777 Probe #22
C 430	14.2	71.0	479	5	RAI02234	Aai02234 Probe #22	C 503	13.8	69.0	333	8	RAI02234	Aai02234 Probe #22
C 431	14.2	71.0	489	10	ADB55762	Adb55762 Toxicity	C 504	13.8	69.0	336	8	ADB55762	Adb55762 Toxicity
C 432	14.2	71.0	489	10	ADB50342	Adb50342 Primary r	C 505	13.8	69.0	337	2	ADB50342	Adb50342 Primary r
C 433	14.2	71.0	516	9	ACH17271	Ach17271 Human adu	C 506	13.8	69.0	337	2	ACH17271	Ach17271 Human adu
C 434	14.2	71.0	687	2	AAV88511	Aav88511 EST clone	C 507	13.8	69.0	337	2	AAV88511	Aav88511 EST clone
C 435	14.2	71.0	865	2	AAZ17705	Aaz17705 Human gen	C 508	13.8	69.0	341	4	AAZ17705	Aaz17705 Human gen
C 436	14.2	71.0	1089	10	ADH82402	Adh82402 Enterococ	C 509	13.8	69.0	372	10	ADH82402	Adh82402 Enterococ
C 437	14.2	71.0	1132	8	ABX95079	Abx95079 Murine AL	C 510	13.8	69.0	372	10	ABX95079	Abx95079 Murine AL
C 438	14.2	71.0	1576	6	AAH15422	Aah15422 Human cDN	C 511	13.8	69.0	382	5	AAH15422	Aah15422 Human cDN
C 439	14.2	71.0	1602	10	ACF68675	Adc68675 Phototrab	C 512	13.8	69.0	384	2	ACF68675	Adc68675 Phototrab
C 440	14.2	71.0	2094	4	ABL020545	Ab120545 Drosophil	C 513	13.8	69.0	388	6	ABL020545	Ab120545 Drosophil
C 441	14.2	71.0	2165	4	ABL05491	Ab105491 Drosophil	C 514	13.8	69.0	388	6	ABL05491	Ab105491 Drosophil
C 442	14.2	71.0	2285	8	ABF32700	Abf32700 Human sec	C 515	13.8	69.0	390	6	ABF32700	Abf32700 Human sec
C 443	14.2	71.0	2285	8	ABZ73401	Abz73401 Secreted	C 516	13.8	69.0	405	3	ABZ73401	Abz73401 Secreted
C 444	14.2	71.0	2285	8	ADA43884	Ada43884 Human sec	C 517	13.8	69.0	405	3	ADA43884	Ada43884 Human sec
C 445	14.2	71.0	2564	4	ABL05488	Ab105488 Drosophil	C 518	13.8	69.0	408	10	ABL05488	Ab105488 Drosophil
C 446	14.2	71.0	2913	5	AAH89402	Aah89402 DNA encod	C 519	13.8	69.0	424	10	AAH89402	Aah89402 DNA encod
C 447	14.2	71.0	2913	5	AAH89402	Aah89402 DNA encod	C 520	13.8	69.0	424	10	AAH89402	Aah89402 DNA encod
C 448	14.2	71.0	3514	2	AAV70359	Aav70359 Human ehb	C 521	13.8	69.0	425	9	AAV70359	Aav70359 Human ehb
C 449	14.2	71.0	3733	4	AAO02704	Aao02704 Human gly	C 522	13.8	69.0	426	3	AAO02704	Aao02704 Human gly
C 450	14.2	71.0	3762	10	ADE07815	Adg07815 Novel cod	C 523	13.8	69.0	427	8	ADE07815	Adg07815 Novel cod
C 451	14.2	71.0	4133	8	ABX49551	Abx49551 Human cDN	C 524	13.8	69.0	429	3	ABX49551	Abx49551 Human cDN
C 452	14.2	71.0	4490	4	AAH02953	Aah02953 Human she	C 525	13.8	69.0	432	12	AAH02953	Aah02953 Human she
C 453	14.2	71.0	4599	4	AAO02702	Aao02702 Human gly	C 526	13.8	69.0	441	4	AAO02702	Aao02702 Human gly
C 454	14.2	71.0	5145	5	ADL45720	Adl45720 Human ova	C 527	13.8	69.0	452	3	ADL45720	Adl45720 Human ova
C 455	14.2	71.0	5145	10	ADE07325	Adro7325 Novel cod	C 528	13.8	69.0	456	10	ADE07325	Adro7325 Novel cod
C 456	14.2	71.0	5957	11	ADL22645	Adl22645 Human dis	C 529	13.8	69.0	460	8	ADL22645	Adl22645 Human dis
C 457	14.2	71.0	9528	10	AAH50032	Aah50032 Human nov	C 530	13.8	69.0	476	3	AAH50032	Aah50032 Human nov
C 458	14.2	71.0	12462	4	ABL05490	Ab105490 Drosophil	C 531	13.8	69.0	479	3	ABL05490	Ab105490 Drosophil
C 459	14.2	71.0	12481	4	ABL20544	Ab120544 Drosophil	C 532	13.8	69.0	482	3	ABL20544	Ab120544 Drosophil

C 533	13.8	69.0	492	5	ABV49261	Abv49261 Human pro	606	13.8	69.0	1000	4	AAf91404	AAf91404 N. mening
C 534	13.8	69.0	509	6	ABL38384	AbL38384 Human col	C 607	13.8	69.0	1000	4	AAf91399	AAf91399 N. mening
C 535	13.8	69.0	526	3	AAZ54437	Aaz54437 Neisseria	C 608	13.8	69.0	1000	6	ABK37762	ABK37762 DNA sequ
C 536	13.8	69.0	537	4	AAF91400	Aaf91400 N. mening	C 609	13.8	69.0	1000	6	ABK37784	ABK37784 DNA sequ
C 537	13.8	69.0	537	6	ABK37780	Abk37780 Strong pr	C 610	13.8	69.0	1000	6	ABK37779	ABK37779 DNA sequ
C 538	13.8	69.0	549	6	ABQ67589	Abq67589 Listeria	C 611	13.8	69.0	1020	10	ADP75238	Adp75238 Thale cre
C 539	13.8	69.0	551	3	AAZ80730	Aaz80730 Human col	C 612	13.8	69.0	1020	12	ADN73012	Adn73012 Thale cre
C 540	13.8	69.0	558	6	AAZ97270	Aaz97270 Neisseria	C 613	13.8	69.0	1037	3	AAa81754	Aaa81754 N. mening
C 541	13.8	69.0	568	4	AAH10489	Aah10489 Human	C 614	13.8	69.0	1065	10	ABZ40089	Abz40089 N. gonorr
C 542	13.8	69.0	567	10	ABX08153	Abx08153 S. pneumo	C 615	13.8	69.0	1113	8	ACA41658	ACA41658 Prokaryot
C 543	13.8	69.0	589	2	AAZ90874	Aaz90874 Providenc	C 616	13.8	69.0	1116	8	ACA24230	ACA24230 Prokaryot
C 544	13.8	69.0	589	8	ABZ54694	Abz54694 Aspergill	C 617	13.8	69.0	1172	10	ADB85157	Adb85157 Rat H2A.1
C 545	13.8	69.0	602	2	AAV09840	Aav09840 Gene No.	C 618	13.8	69.0	1183	4	AAI86728	Aai86728 Human pol
C 546	13.8	69.0	607	4	AAZ84920	Aaz84920 I. ricinu	C 619	13.8	69.0	1184	3	AAZ50834	Aaz50834 Arabidops
C 547	13.8	69.0	611	3	AAZ42590	Aaz42590 Arabidops	C 620	13.8	69.0	1184	3	AAZ36340	Aaz36340 Arabidops
C 548	13.8	69.0	619	3	AAZ52019	Aaz52019 Arabidops	C 621	13.8	69.0	1200	8	ACA24536	ACA24536 Prokaryot
C 549	13.8	69.0	621	6	ABN61077	Abn61077 Human can	C 622	13.8	69.0	1209	8	ACA22138	ACA22138 Prokaryot
C 550	13.8	69.0	646	3	AAAF11871	Aaf11871 Aspergill	C 623	13.8	69.0	1217	10	ACC60679	Acc60679 Gene sequ
C 551	13.8	69.0	663	10	ADB51877	Adb51877 Primary r	C 624	13.8	69.0	1218	8	ACA43055	ACA43055 Prokaryot
C 552	13.8	69.0	673	12	ADT45607	Adt45607 Wheat iso	C 625	13.8	69.0	1230	8	ACA43076	ACA43076 Prokaryot
C 553	13.8	69.0	693	8	ACA41804	Aca41804 Prokaryot	C 626	13.8	69.0	1237	3	AAZ59111	Aaz59111 Human sec
C 554	13.8	69.0	697	5	AAH68584	Aah68584 Human pro	C 627	13.8	69.0	1237	8	ABZ73295	Abz73295 Secreted
C 555	13.8	69.0	703	2	AAZ40821	Aaz40821 Secreted	C 628	13.8	69.0	1237	8	ADA97916	Ada97916 Human sec
C 556	13.8	69.0	703	3	AAA81857	Aaa81857 N. mening	C 629	13.8	69.0	1237	10	ADC20076	Adc20076 Human sec
C 557	13.8	69.0	703	11	ADM77798	Adm77798 Human cdn	C 630	13.8	69.0	1237	10	ABZ66909	Abz66909 Human sec
C 558	13.8	69.0	703	12	ADP19119	Adp19119 Human sec	C 631	13.8	69.0	1318	9	ADA27598	Ada27598 Human sta
C 559	13.8	69.0	720	6	ABQ69576	Abq69576 Listeria	C 632	13.8	69.0	1346	10	ADE63372	Ade63372 Rat Gene
C 560	13.8	69.0	728	6	ABK14745	Abk14745 Human den	C 633	13.8	69.0	1347	10	ADE49742	Ade49742 Teosinte
C 561	13.8	69.0	747	6	ABK79429	Abk79429 Bacillus	C 634	13.8	69.0	1347	10	ADE83993	Ade83993 Chapulte E
C 562	13.8	69.0	748	3	AAA81785	Aaa81785 N. mening	C 635	13.8	69.0	1385	8	ABX05341	Abx05341 Human nov
C 563	13.8	69.0	749	4	AAK65005	Aak65005 Human imm	C 636	13.8	69.0	1385	8	ABX09851	Abx09851 N. mening
C 564	13.8	69.0	750	8	ACA41827	Aca41827 Prokaryot	C 637	13.8	69.0	1416	10	ADG20423	Adg20423 Lentinula
C 565	13.8	69.0	756	6	ABQ67677	Abq67677 Listeria	C 638	13.8	69.0	1428	8	ACA39434	Aca39434 Prokaryot
C 566	13.8	69.0	757	4	AAK56863	Aak56863 Human imm	C 639	13.8	69.0	1473	3	AAZ48699	Aaz48699 Arabidops
C 567	13.8	69.0	760	11	ADP65795	Adp65795 Human BM-	C 640	13.8	69.0	1475	3	AAZ32775	Aaz32775 Arabidops
C 568	13.8	69.0	760	11	ADP65714	Adp65714 Human pla	C 641	13.8	69.0	1558	2	AAV29471	Aav29471 Orpinomyc
C 569	13.8	69.0	760	12	ADJ75256	Adj75256 Marker ge	C 642	13.8	69.0	1561	12	ADG32137	Adg32137 DNA encod
C 570	13.8	69.0	760	12	ADN43099	Adn43099 DNA encod	C 643	13.8	69.0	1580	10	ABZ22026	Abz22026 Catalpa o
C 571	13.8	69.0	760	12	ADQ20100	Ado20100 Human PRO	C 644	13.8	69.0	1638	3	AAA81788	Aaa81788 N. mening
C 572	13.8	69.0	762	2	AAZ17581	Aaz17581 Human gen	C 645	13.8	69.0	1660	2	AAV43012	Aav43012 Streptoco
C 573	13.8	69.0	764	8	ABX77651	Abx77651 Different	C 646	13.8	69.0	1660	2	AAZ96373	Aaz96373 S. pneumo
C 574	13.8	69.0	786	10	ABZ38306	Abz38306 N. gonorr	C 647	13.8	69.0	1672	10	ADE49741	Ade49741 Teosinte
C 575	13.8	69.0	795	3	AAZ16098	Aaz16098 Human gen	C 648	13.8	69.0	1672	10	ADE83992	Ade83992 Chapulte E
C 576	13.8	69.0	795	3	AAA64336	Aaa64336 Clone 279	C 649	13.8	69.0	1699	3	AAa81539	Aaa81539 N. mening
C 577	13.8	69.0	798	8	ABX77650	Abx77650 Different	C 650	13.8	69.0	1731	10	ADG10603	Adg10603 Human STA
C 578	13.8	69.0	803	6	AAZ62750	Aaz62750 cDNA sequ	C 651	13.8	69.0	1756	6	AAZ43228	Aaz43228 Human BS2
C 579	13.8	69.0	804	8	ABZ51029	Abz51029 Aspergill	C 652	13.8	69.0	1756	6	ADA00861	Ada00861 Human bre
C 580	13.8	69.0	807	2	AAQ32905	Aaq32905 BLAP (S3T)	C 653	13.8	69.0	1760	6	ADA43227	Ada43227 Human BS2
C 581	13.8	69.0	807	2	AAQ32922	Aaq32922 BLAP (S3T)	C 654	13.8	69.0	1760	9	ADA00860	Ada00860 Human bre
C 582	13.8	69.0	807	2	AAQ32910	Aaq32910 BLAP (S3T)	C 655	13.8	69.0	1788	6	ABL89559	AbL89559 Human pol
C 583	13.8	69.0	807	2	AAQ98739	Aaq98739 DNA encod	C 656	13.8	69.0	1791	4	AAf74270	Aaf74270 Carrot ca
C 584	13.8	69.0	807	2	AAZ70317	Aaz70317 Mutant BL	C 657	13.8	69.0	1794	6	ABZ32308	Abz32308 Candida a
C 585	13.8	69.0	813	8	ACA40063	Aca40063 Prokaryot	C 658	13.8	69.0	1837	6	ABT07703	Abt07703 Breast ca
C 586	13.8	69.0	822	3	AAA81751	Aaa81751 N. mening	C 659	13.8	69.0	1837	9	ADA27592	Ada27592 Human eta
C 587	13.8	69.0	822	8	ACA41915	Aca41915 Prokaryot	C 660	13.8	69.0	1850	2	AAV09251	Aav09251 Cytochrom
C 588	13.8	69.0	837	3	AAZ53289	Aaz53289 Neisseria	C 661	13.8	69.0	1850	2	AAV12203	Aav12203 Zebrafish
C 589	13.8	69.0	861	8	ABZ51670	Abz51670 Aspergill	C 662	13.8	69.0	1850	4	AAH22442	Aah22442 Zebrafish
C 590	13.8	69.0	864	3	AAZ76775	Aaz76775 Human ORF	C 663	13.8	69.0	1850	6	AAQ74193	Aaq74193 Zebrafish
C 591	13.8	69.0	870	3	AAA81780	Aaa81780 N. mening	C 664	13.8	69.0	1850	6	AAZ24484	Aaz24484 Zebrafish
C 592	13.8	69.0	880	2	AAZ06794	Aaz06794 CGA-1 (ch	C 665	13.8	69.0	1868	6	ABZ55143	Abz55143 Human cdn
C 593	13.8	69.0	891	3	AAZ98118	Aaz98118 Human col	C 666	13.8	69.0	1872	8	ADA67803	Ada67803 Arabidops
C 594	13.8	69.0	897	4	AAZ3664	Aaz3664 Human cdn	C 667	13.8	69.0	1887	4	AAH53725	Aah53725 S. epider
C 595	13.8	69.0	897	4	AAZ36003	Aaz36003 Human cdn	C 668	13.8	69.0	1890	6	ABN92094	Abn92094 Staphyloc
C 596	13.8	69.0	897	12	ADL30091	Adl30091 3' end of	C 669	13.8	69.0	1893	12	ADJ34825	Adj34825 DNA encod
C 597	13.8	69.0	897	12	ADL28430	Adl28430 5' end of	C 670	13.8	69.0	1896	10	ADF23255	Adf23255 AT931670
C 598	13.8	69.0	903	3	AAA81946	Aaa81946 N. mening	C 671	13.8	69.0	1900	8	ABZ82389	Abz82389 Perennial
C 599	13.8	69.0	906	4	ABL02209	AbL02209 Drosophil	C 672	13.8	69.0	1919	3	AAZ81713	Aaz81713 Human sec
C 600	13.8	69.0	916	3	AAA82186	Aaa82186 N. mening	C 673	13.8	69.0	1919	8	ABZ73444	Abz73444 Secreted
C 601	13.8	69.0	924	6	ABX77302	Abx77302 Bacillus	C 674	13.8	69.0	1919	8	ADA43905	Ada43905 Human sec
C 602	13.8	69.0	924	6	AAf91381	Aaf91381 N. mening	C 675	13.8	69.0	1919	10	ADC20166	Adc20166 Human sec
C 603	13.8	69.0	924	6	ABK37761	Abk37761 DNA sequ	C 676	13.8	69.0	1919	10	ABT18809	Abt18809 Human sec
C 604	13.8	69.0	933	10	ADH84224	Adh84224 Enterococ	C 677	13.8	69.0	1919	10	ABZ67051	Abz67051 Human sec
C 605	13.8	69.0	1000	4	AAf91382	Aaf91382 N. mening	C 678	13.8	69.0	1922	3	AAZ42231	Aaz42231 Arabidops

679	13.8	69.0	1932	10	ADK4835	Adk4835 Disease t	752	13.8	69.0	5998	6	ABS98851	AbS98851 Enterococ
680	13.8	69.0	1942	4	AAH15669	Aah15669 Human cdn	753	13.8	69.0	6616	4	ABL04366	AbI04366 Drosophil
681	13.8	69.0	1957	10	ADF75266	Adf75266 Thale cre	754	13.8	69.0	6638	4	ABL02932	AbI02932 Drosophil
682	13.8	69.0	1953	8	ACA29707	AcA29707 Prokaryot	755	13.8	69.0	6794	4	ABL16438	AbI16438 Drosophil
683	13.8	69.0	1968	8	ACA33301	AcA33301 Prokaryot	756	13.8	69.0	7162	2	AAV22214	AAV22214 Mouse Cdx
684	13.8	69.0	2000	6	ABZ16499	Abz16499 Arabidops	757	13.8	69.0	7219	5	AAV22247	AAV22247 Mouse DNA
685	13.8	69.0	2000	6	ABZ15235	Abz15235 Arabidops	758	13.8	69.0	7219	6	ABS67550	ABs67550 Novel hum
686	13.8	69.0	2000	8	ADA72342	Ada72342 Rice gene	759	13.8	69.0	7313	2	AAV29268	AAV29268 Nucleotid
687	13.8	69.0	2034	12	ADL04094	Adl04094 DNA encod	760	13.8	69.0	7800	3	AAA81496	AAa81496 N. mening
688	13.8	69.0	2045	5	AA89018	Aas89018 DNA encod	761	13.8	69.0	7959	3	AAA81510	AAa81510 N. mening
689	13.8	69.0	2132	3	AA81546	Aa81546 N. mening	762	13.8	69.0	8020	4	ABL22894	AbL22894 Drosophil
690	13.8	69.0	2132	3	AA81546	Aa81546 N. mening	763	13.8	69.0	8059	3	AA81747	AAa81747 N. mening
691	13.8	69.0	2142	4	AA81546	Aa81546 N. mening	764	13.8	69.0	8183	3	AA81524	AAa81524 N. mening
692	13.8	69.0	2181	12	ADN73118	Adn73118 Thale cre	765	13.8	69.0	9133	3	AAA81730	AAa81730 N. mening
693	13.8	69.0	2245	4	AA816818	Aa816818 Paenibaci	766	13.8	69.0	9243	3	AAA81534	AAa81534 N. mening
694	13.8	69.0	2343	3	AAA81763	Aa81763 N. mening	767	13.8	69.0	9316	4	ABL27862	AbL27862 Drosophil
695	13.8	69.0	2380	6	ABT10174	Abt10174 Human bre	768	13.8	69.0	9579	4	ABL17086	AbL17086 Drosophil
696	13.8	69.0	2380	6	ABX76344	Abx76344 Lung canc	769	13.8	69.0	9579	4	ABL19834	AbL19834 Drosophil
697	13.8	69.0	2380	8	ACC50302	Acc50302 Breast ca	770	13.8	69.0	9688	4	ABL10370	AbL10370 Drosophil
698	13.8	69.0	2380	10	ADB80515	Adb80515 Ovarian c	771	13.8	69.0	9688	4	ABL20196	AbL20196 Drosophil
699	13.8	69.0	2380	10	ADD12708	Add12708 Human cdn	772	13.8	69.0	9948	4	ABL10538	AbL10538 Drosophil
700	13.8	69.0	2380	11	ADN38781	Adn38781 Cancer/an	773	13.8	69.0	9941	3	AAA81461	AAa81461 N. mening
701	13.8	69.0	2380	12	ADO28590	Ado28590 Human sta	774	13.8	69.0	9941	3	AAA81461	AAa81461 N. mening
702	13.8	69.0	2387	6	ABL90673	AbI90673 Human pol	775	13.8	69.0	10214	2	AAV52162	AAV52162 Streptoco
703	13.8	69.0	2397	12	ACH92153	Ach92153 Human gen	776	13.8	69.0	10254	2	AAV52162	AAV52162 Streptoco
704	13.8	69.0	2404	4	AAK94911	Aak94911 Human ful	777	13.8	69.0	11243	3	AA81738	AAa81738 N. mening
705	13.8	69.0	2404	12	ADL32103	Adl32103 Full leng	778	13.8	69.0	11243	3	AA81738	AAa81738 N. mening
706	13.8	69.0	2426	4	ABL24748	AbI24748 Drosophil	779	13.8	69.0	11658	3	AAA81506	AAa81506 N. mening
707	13.8	69.0	2428	11	ADMO1635	Admo1635 Human cdn	780	13.8	69.0	11658	3	AAA81506	AAa81506 N. mening
708	13.8	69.0	2512	9	ACD19048	Act19048 E. coli o	781	13.8	69.0	11693	4	ABL30327	AbL30327 Drosophil
709	13.8	69.0	2556	12	ADJ40509	Adj40509 Plant cdn	782	13.8	69.0	12077	3	AAA81734	AAa81734 N. mening
710	13.8	69.0	2600	2	AAT42127	Aat42127 Neisseria	783	13.8	69.0	12077	3	AAA81734	AAa81734 N. mening
711	13.8	69.0	2600	4	AAH10201	Aah10201 N. gonorr	784	13.8	69.0	12893	3	AAA81733	AAa81733 N. mening
712	13.8	69.0	2600	6	ABS67385	Abs67385 Neisseria	785	13.8	69.0	12893	3	AAA81733	AAa81733 N. mening
713	13.8	69.0	2600	9	ADA44891	Ada44891 N. gonorr	786	13.8	69.0	13011	2	AAT96631	Aat96631 CDNA enco
714	13.8	69.0	2663	12	ADL27235	Adl27235 Nucleotid	787	13.8	69.0	13011	10	ABT42448	Abt42448 Toxicity
715	13.8	69.0	2663	4	ABL10539	AbI10539 Drosophil	788	13.8	69.0	13011	12	ADP72914	Adp72914 Renal tox
716	13.8	69.0	2677	4	ABL22446	AbI22446 Drosophil	789	13.8	69.0	13274	4	ABL05526	AbL05526 Drosophil
717	13.8	69.0	2695	4	ABL02360	AbI02360 Drosophil	790	13.8	69.0	13423	3	AAA81529	AAa81529 N. mening
718	13.8	69.0	2751	8	ACA52436	AcA52436 Prokaryot	791	13.8	69.0	13574	3	AAA81529	AAa81529 N. mening
719	13.8	69.0	2829	11	ABD01036	Abd01036 Klebsiell	792	13.8	69.0	13574	3	AAA81529	AAa81529 N. mening
720	13.8	69.0	2868	4	AAK94441	Aak94441 Human ful	793	13.8	69.0	13732	3	AAA81484	AAa81484 N. mening
721	13.8	69.0	2868	5	AA813642	Aa813642 cDNA sequ	794	13.8	69.0	13786	3	AAA81480	AAa81480 N. mening
722	13.8	69.0	2868	12	ADL31197	Adl31197 Full leng	795	13.8	69.0	13786	3	AAA81480	AAa81480 N. mening
723	13.8	69.0	2906	4	ABL02208	AbL02208 Drosophil	796	13.8	69.0	13894	10	ACC63517	Acc63517 Mycoplasm
724	13.8	69.0	3114	4	AAH54060	Aah54060 S. epider	797	13.8	69.0	13894	10	ACC63517	Acc63517 Mycoplasm
725	13.8	69.0	3155	4	AAH54060	Aah54060 S. epider	798	13.8	69.0	13894	12	ADN48952	Adn48952 Mycoplasm
726	13.8	69.0	3404	9	ACD19081	Act19081 E. coli o	799	13.8	69.0	13894	12	ADN48952	Adn48952 Mycoplasm
727	13.8	69.0	3580	4	AAH53993	Aah53993 S. epider	800	13.8	69.0	15620	4	ABL03526	AbL03526 Drosophil
728	13.8	69.0	3580	4	AAH53993	Aah53993 S. epider	801	13.8	69.0	15620	4	ABL03526	AbL03526 Drosophil
729	13.8	69.0	3696	4	AAH53993	Aah53993 S. epider	802	13.8	69.0	15896	3	AAA81517	AAa81517 N. mening
730	13.8	69.0	3696	4	AAH53993	Aah53993 S. epider	803	13.8	69.0	16677	3	AAA81519	AAa81519 N. mening
731	13.8	69.0	4017	10	ADG10605	Adg10605 Human stru	804	13.8	69.0	16878	3	AAA81515	AAa81515 N. mening
732	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	805	13.8	69.0	17381	3	AAA81493	AAa81493 N. mening
733	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	806	13.8	69.0	17381	3	AAA81493	AAa81493 N. mening
734	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	807	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
735	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	808	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
736	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	809	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
737	13.8	69.0	4055	12	ADG10605	Adg10605 Human stru	810	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
738	13.8	69.0	4172	4	ABL12206	AbL12206 Drosophil	811	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
739	13.8	69.0	4172	4	ABL12206	AbL12206 Drosophil	812	13.8	69.0	18920	4	ABL02306	AbL02306 Drosophil
740	13.8	69.0	4298	4	AAH17879	Aah17879 Human cdn	813	13.8	69.0	19374	3	AAA81485	AAa81485 N. mening
741	13.8	69.0	4335	5	ADL46060	Adl46060 Human ova	814	13.8	69.0	19374	3	AAA81485	AAa81485 N. mening
742	13.8	69.0	4335	5	ADL46060	Adl46060 Human ova	815	13.8	69.0	20352	3	AAA81488	AAa81488 N. mening
743	13.8	69.0	4583	4	AA815441	Aa815441 N. mening	816	13.8	69.0	20352	3	AAA81488	AAa81488 N. mening
744	13.8	69.0	4594	4	AAK81445	Aak81445 Human imm	817	13.8	69.0	20844	3	AAA81460	AAa81460 N. mening
745	13.8	69.0	4594	4	AAK81445	Aak81445 Human imm	818	13.8	69.0	20844	3	AAA81460	AAa81460 N. mening
746	13.8	69.0	4927	3	AA81466	Aa81466 N. mening	819	13.8	69.0	21091	3	AAA81523	AAa81523 N. mening
747	13.8	69.0	4927	3	AA81466	Aa81466 N. mening	820	13.8	69.0	21091	3	AAA81523	AAa81523 N. mening
748	13.8	69.0	5317	4	ABL17087	AbL17087 Drosophil	821	13.8	69.0	21294	2	AA81477	AAa81477 N. mening
749	13.8	69.0	5452	12	ADQ23610	Adq23610 Human sof	822	13.8	69.0	21294	2	AA81477	AAa81477 N. mening
750	13.8	69.0	5532	3	AAA81538	AAa81538 N. mening	823	13.8	69.0	21294	2	AA81477	AAa81477 N. mening
751	13.8	69.0	5538	4	AAK67569	Aak67569 Human imm	824	13.8	69.0	21294	2	AA81477	AAa81477 N. mening
752	13.8	69.0	5598	2	AAH13056	Aah13056 Enterococ	825	13.8	69.0	21294	2	AA81477	AAa81477 N. mening

C 825	13.8	69.0	30078	3	AAA81520	AAA81520 N. mening	AAA81520 N. mening	C 898	13.8	69.0	110000	3	AAA81490_03	Continuation (4 of
C 826	13.8	69.0	30078	3	AAA81520	AAA81520 N. mening	AAA81520 N. mening	899	13.8	69.0	110000	3	AAA81490_04	Continuation (5 of
C 827	13.8	69.0	31562	4	ABL03868	Drosophila	ABL03868 Drosophila	C 900	13.8	69.0	110000	3	AAA81490_05	Continuation (6 of
C 828	13.8	69.0	33303	3	AAA81514	N. mening	AAA81514 N. mening	C 901	13.8	69.0	110000	3	AAA81490_06	Continuation (7 of
C 829	13.8	69.0	33962	3	AAA81528	N. mening	AAA81528 N. mening	C 902	13.8	69.0	110000	3	AAA81490_07	Continuation (8 of
C 830	13.8	69.0	33962	3	AAA81528	N. mening	AAA81528 N. mening	C 903	13.8	69.0	110000	3	AAA81490_08	Continuation (9 of
C 831	13.8	69.0	34775	12	ADM43182	Wild-type	ADM43182 Wild-type	C 904	13.8	69.0	110000	3	AAA81490_09	Continuation (10 of
C 832	13.8	69.0	34793	6	ABQ76121	Adenovirus	ABQ76121 Adenovirus	C 905	13.8	69.0	110000	3	AAA81490_10	Continuation (11 of
C 833	13.8	69.0	34794	5	ACAC8884	Ad35 nucle	ACAC8884 Ad35 nucle	C 906	13.8	69.0	110000	3	AAA81490_11	Continuation (12 of
C 834	13.8	69.0	34794	5	ABT08275	Human ade	ABT08275 Human ade	C 907	13.8	69.0	110000	3	AAA81490_12	Continuation (13 of
C 835	13.8	69.0	34794	12	ADH23244	Human ade	ADH23244 Human ade	C 908	13.8	69.0	110000	3	AAA81490_13	Continuation (14 of
C 836	13.8	69.0	34796	12	ADM43171	Wild-type	ADM43171 Wild-type	C 909	13.8	69.0	110000	3	AAA81490_14	Continuation (15 of
C 837	13.8	69.0	35042	3	AAA81454	N. mening	AAA81454 N. mening	C 910	13.8	69.0	110000	3	AAA81490_15	Continuation (16 of
C 838	13.8	69.0	35133	3	AAA81518	N. mening	AAA81518 N. mening	C 911	13.8	69.0	110000	3	AAA81490_16	Continuation (17 of
C 839	13.8	69.0	36159	6	ABN85329	Human kin	ABN85329 Human kin	C 912	13.8	69.0	110000	3	AAA81490_17	Continuation (18 of
C 840	13.8	69.0	36471	3	AAA81453	N. mening	AAA81453 N. mening	C 913	13.8	69.0	110000	3	AAA81490_18	Continuation (19 of
C 841	13.8	69.0	36471	3	AAA81453	N. mening	AAA81453 N. mening	C 914	13.8	69.0	110000	3	AAA81490_19	Continuation (20 of
C 842	13.8	69.0	37096	3	AAA81489	N. mening	AAA81489 N. mening	C 915	13.8	69.0	110000	3	AAA81490_20	Continuation (21 of
C 843	13.8	69.0	37668	3	AAA81490_14	Continuation (15 of	Continuation (15 of	C 916	13.8	69.0	110000	3	AAA81490_21	Continuation (22 of
C 844	13.8	69.0	37668	3	AAA81490_14	Continuation (15 of	Continuation (15 of	C 917	13.8	69.0	110000	3	AAA81490_22	Continuation (23 of
C 845	13.8	69.0	37948	3	AAZ06831	Photophab	AAZ06831 Photophab	C 918	13.8	69.0	110000	3	AAA81490_23	Continuation (24 of
C 846	13.8	69.0	37996	4	ABL07876	Drosophila	ABL07876 Drosophila	C 919	13.8	69.0	110000	3	AAA81490_24	Continuation (25 of
C 847	13.8	69.0	39824	10	ADCC0831	Enterohae	ADCC0831 Enterohae	C 920	13.8	69.0	110000	3	AAA81490_25	Continuation (26 of
C 848	13.8	69.0	44608	3	AAA81495	N. mening	AAA81495 N. mening	C 921	13.8	69.0	110000	3	AAA81490_26	Continuation (27 of
C 849	13.8	69.0	44861	6	AAAS20000	DNA encod	AAAS20000 DNA encod	C 922	13.8	69.0	110000	3	AAA81490_27	Continuation (28 of
C 850	13.8	69.0	45774	12	ADJ12457	DNA fragm	ADJ12457 DNA fragm	C 923	13.8	69.0	110000	3	AAA81490_28	Continuation (29 of
C 851	13.8	69.0	46593	3	AAA81456	N. mening	AAA81456 N. mening	C 924	13.8	69.0	110000	3	AAA81490_29	Continuation (30 of
C 852	13.8	69.0	46593	3	AAA81456	N. mening	AAA81456 N. mening	C 925	13.8	69.0	110000	3	AAA81490_30	Continuation (31 of
C 853	13.8	69.0	47475	3	AAA81465	N. mening	AAA81465 N. mening	C 926	13.8	69.0	110000	3	AAA81490_31	Continuation (32 of
C 854	13.8	69.0	48275	3	AAA81501	N. mening	AAA81501 N. mening	C 927	13.8	69.0	110000	3	AAA81490_32	Continuation (33 of
C 855	13.8	69.0	48275	3	AAA81501	N. mening	AAA81501 N. mening	C 928	13.8	69.0	110000	3	AAA81490_33	Continuation (34 of
C 856	13.8	69.0	49646	3	AAA81457	N. mening	AAA81457 N. mening	C 929	13.8	69.0	110000	3	AAA81490_34	Continuation (35 of
C 857	13.8	69.0	49646	3	AAA81457	N. mening	AAA81457 N. mening	C 930	13.8	69.0	110000	3	AAA81490_35	Continuation (36 of
C 858	13.8	69.0	49650	10	ADCC0365	Enterohae	ADCC0365 Enterohae	C 931	13.8	69.0	110000	6	ABQ67196_2	Continuation (37 of
C 859	13.8	69.0	49767	3	AAA81458	N. mening	AAA81458 N. mening	C 932	13.8	69.0	110000	6	ABQ69245_16	Continuation (38 of
C 860	13.8	69.0	49767	3	AAA81458	N. mening	AAA81458 N. mening	C 933	13.8	69.0	110000	6	ABQ69245_16	Continuation (39 of
C 861	13.8	69.0	50925	3	AAA81487	N. mening	AAA81487 N. mening	C 934	13.8	69.0	110000	6	ABQ67195_1	Continuation (40 of
C 862	13.8	69.0	50925	3	AAA81487	N. mening	AAA81487 N. mening	C 935	13.8	69.0	110000	10	ADF77343_09	Continuation (41 of
C 863	13.8	69.0	52253	3	AAA81478	N. mening	AAA81478 N. mening	C 936	13.8	69.0	110000	10	ADF77343_11	Continuation (42 of
C 864	13.8	69.0	52253	3	AAA81478	N. mening	AAA81478 N. mening	C 937	13.8	69.0	110000	12	ADN46845_18	Continuation (43 of
C 865	13.8	69.0	56485	3	AAA81476	N. mening	AAA81476 N. mening	C 938	13.8	69.0	110000	12	ADN46845_19	Continuation (44 of
C 866	13.8	69.0	56485	3	AAA81476	N. mening	AAA81476 N. mening	C 939	13.8	69.0	110000	12	ADN47591_01	Continuation (45 of
C 867	13.8	69.0	56609	3	AAA81459	N. mening	AAA81459 N. mening	C 940	13.8	69.0	110000	12	ADN46123_18	Continuation (46 of
C 868	13.8	69.0	56609	3	AAA81459	N. mening	AAA81459 N. mening	C 941	13.8	69.0	110000	12	ADN46123_19	Continuation (47 of
C 869	13.8	69.0	60873	3	AAA81459	N. mening	AAA81459 N. mening	C 942	13.8	69.0	110000	12	ADN47203_01	Continuation (48 of
C 870	13.8	69.0	62598	10	ABSS6454_21	Continuation (22 of	Continuation (22 of	C 943	13.8	69.0	110000	12	ADN46464_18	Continuation (49 of
C 871	13.8	69.0	63563	4	AAAF28546	Genomic f	AAAF28546 Genomic f	C 944	13.8	69.0	110000	12	ADN46464_19	Continuation (50 of
C 872	13.8	69.0	65632	3	AAA81502	N. mening	AAA81502 N. mening	C 945	13.8	69.0	110000	12	ADN47960_01	Continuation (51 of
C 873	13.8	69.0	69936	3	AAA81479	N. mening	AAA81479 N. mening	C 946	13.8	69.0	110000	12	ADO79173_2	Continuation (52 of
C 874	13.8	69.0	69936	3	AAA81479	N. mening	AAA81479 N. mening	C 947	13.8	69.0	110000	12	ADO79173_3	Continuation (53 of
C 875	13.8	69.0	70768	6	AAAL41152	Wooden le	AAAL41152 Wooden le	C 948	13.8	69.0	128139	6	AAI64291	Continuation (54 of
C 876	13.8	69.0	72750	3	AAA81468	N. mening	AAA81468 N. mening	C 949	13.8	69.0	133719	3	AAI64291	Continuation (55 of
C 877	13.8	69.0	72750	3	AAA81468	N. mening	AAA81468 N. mening	C 950	13.8	69.0	141912	10	ADC86530	Continuation (56 of
C 878	13.8	69.0	78845	3	AAA81463	N. mening	AAA81463 N. mening	C 951	13.8	69.0	147309	6	ABK49450	Continuation (57 of
C 879	13.8	69.0	92934	3	AAA81473	N. mening	AAA81473 N. mening	C 952	13.8	69.0	172325	3	AAAF21613	Continuation (58 of
C 880	13.8	69.0	96596	10	ADCC95287	Mouse Fis	ADCC95287 Mouse Fis	C 953	13.8	69.0	177851	8	AAI57272	Continuation (59 of
C 881	13.8	69.0	96597	10	ADCC95287	Mouse Fis	ADCC95287 Mouse Fis	C 954	13.8	69.0	349980	3	AAAF21607	Continuation (60 of
C 882	13.8	69.0	96597	10	ADCC95287	Mouse Fis	ADCC95287 Mouse Fis	C 955	13.8	69.0	349980	3	AAAF21607	Continuation (61 of
C 883	13.8	69.0	96597	12	ADM74402	Murine ca	ADM74402 Murine ca	C 956	13.8	69.0	349980	3	AAAF21609	Continuation (62 of
C 884	13.8	69.0	97662	4	AAAF83908	Genomic s	AAAF83908 Genomic s	C 957	13.8	69.0	349980	3	AAAF21610	Continuation (63 of
C 885	13.8	69.0	101786	3	AAAF22293	BAC conta	AAAF22293 BAC conta	C 958	13.8	69.0	349980	3	AAAF21610	Continuation (64 of
C 886	13.8	69.0	102634	3	AAA81464	N. mening	AAA81464 N. mening	C 959	13.8	69.0	349980	3	AAAF21610	Continuation (65 of
C 887	13.8	69.0	102634	3	AAA81464	N. mening	AAA81464 N. mening	C 960	13.8	69.0	349980	3	AAAF21610	Continuation (66 of
C 888	13.8	69.0	110000	2	AAAT58840_1	Continuation (2 of	Continuation (2 of	C 961	13.8	69.0	349980	3	AAAF21611	Continuation (67 of
C 889	13.8	69.0	110000	2	AAAT58840_2	Continuation (3 of	Continuation (3 of	C 962	13.8	69.0	349980	3	AAAF21611	Continuation (68 of
C 890	13.8	69.0	110000	2	AAAT58840_3	Continuation (4 of	Continuation (4 of	C 963	13.8	69.0	349980	3	AAAF21612	Continuation (69 of
C 891	13.8	69.0	110000	2	AAAT58840_4	Continuation (5 of	Continuation (5 of	C 964	13.8	69.0	349980	3	AAAF21612	Continuation (70 of
C 892	13.8	69.0	110000	3	AAA81490_00	Continuation (2 of	Continuation (2 of	C 965	13.8	69.0	349980	3	AAAF21544	Continuation (71 of
C 893	13.8	69.0	110000	3	AAA81490_01	Continuation (3 of	Continuation (3 of	C 966	13.8	69.0	349980	3	AAAF21544	Continuation (72 of
C 894	13.8	69.0	110000	3	AAA81490_02	Continuation (4 of	Continuation (4 of	C 967	13.8	69.0	349980	3	AAAF21544	Continuation (73 of
C 895	13.8	69.0	110000	3	AAA81490_03	Continuation (5 of	Continuation (5 of	C 968	13.8	69.0	349980	3	AAAF21544	Continuation (74 of
C 896	13.8	69.0	110000	3	AAA81490_04	Continuation (6 of	Continuation (6 of	C 969	13.8	69.0	349980	3	AAAF21544	Continuation (75 of
C 897	13.8	69.0	110000	3	AAA81490_05	Continuation (7 of	Continuation (7 of	C 970	13.8	69.0	349980	3	AAAF21544	Continuation (76 of

971 13.6 68.0 27 3 Aaa97179 Oligonuc1
 972 13.6 68.0 27 3 Aaa08325 IGM-R mu
 973 13.6 68.0 27 4 Aac91958 Human ICA
 974 13.6 68.0 27 6 Abk09368 Monoclonal
 975 13.6 68.0 27 10 Adg25757 Human ICA
 976 13.6 68.0 38 10 Ach00956 Human pap
 977 13.6 68.0 38 10 Ach00935 Human pap
 978 13.6 68.0 56 10 Adc01756 Enterohae
 979 13.6 68.0 60 6 Abn38859 Human spl
 980 13.6 68.0 60 6 Abn50762 Human spl
 981 13.6 68.0 83 12 Ado59849 D-CGRP b1
 982 13.6 68.0 96 10 Abz40709 N. gonorr
 983 13.6 68.0 125 4 Aai23213 Probe #13
 984 13.6 68.0 125 4 Aab68320 Human foe
 985 13.6 68.0 125 4 Aai48534 Probe #17
 986 13.6 68.0 125 4 Aaa50367 Human bre
 987 13.6 68.0 125 4 Aaa35316 Human bre
 988 13.6 68.0 125 4 Aak42459 Human bon
 989 13.6 68.0 125 4 Aak16694 Human bra
 990 13.6 68.0 125 4 Aab42073 Human liv
 991 13.6 68.0 125 5 Aai08859 Probe #88
 992 13.6 68.0 125 6 Abs16511 Human gen
 993 13.6 68.0 184 4 Aai21169 Probe #11
 994 13.6 68.0 184 4 Aaa68250 Human foe
 995 13.6 68.0 184 4 Aai46437 Probe #15
 996 13.6 68.0 184 4 Aab48356 Human bre
 997 13.6 68.0 184 4 Aab33315 Probe #11
 998 13.6 68.0 184 4 Aak40411 Human bon
 999 13.6 68.0 184 4 Aak14666 Human bra
 1000 13.6 68.0 184 4 Abs39973 Human liv

ALIGNMENTS

RESULT 1
 ABN84785
 ID ABN84785 standard; DNA; 20 BP.
 AC ABN84785;
 DT 05-NOV-2002 (first entry)
 DE Primer useful for familial dysautonomia allele genotype analysis.
 DE Familial dysautonomia; Riley-Day syndrome;
 KW hereditary sensory neuropathy III; human; carrier; diagnosis;
 KW IkappaB kinase-complex associated protein; primer; SSCP;
 KW single-strand conformational polymorphism; ss.
 OS Homo sapiens.
 XX
 XX EP1225232-A2.
 XX
 XX PD 24-JUL-2002.
 XX
 XX PF 17-JAN-2002; 2002EP-00001232.
 XX
 XX PR 17-JAN-2001; 2001US-0262284P.
 XX
 XX FA (RUBI/) RUBIN B Y.
 XX FA (ANDE/) ANDERSON S L.
 XX
 XX FI Rubin BY, Anderson SL;
 XX
 XX DR WPI; 2002-601228/65.
 XX
 XX PT Detecting a polymorphism in a gene encoding the IkappaB kinase-complex-
 PT associated protein is used to diagnose and identify carriers of familial
 PT dysautonomia.
 XX
 XX PS Claim 7; Page 9; 16pp; English.
 XX

CC The invention provides a method for detecting a polymorphism linked to a
 CC gene associated with familial dysautonomia (FD). This involves detecting
 CC a disruptive mutation in a gene encoding the IkappaB kinase-complex-
 CC associated protein (IKAP) on chromosome 9q31. Sequence analysis of the
 CC IKAP-encoding gene showed, in chromosomes with the major FD haplotype, a
 CC T to C transition in position 6 of the donor splice site of intron 20.
 CC This mutation (2507+6T to C) results in the generation of an IKAP mRNA in
 CC which exon 20 is spliced out along with intron 20. Sequence analysis of
 CC the IKAP gene of individuals heterozygous for the FD chromosome with the
 CC most common minor haplotype (minor 2) showed a G to C transversion of
 CC nucleotide 2390 in exon 19 of the reported IKAP cDNA, resulting in an
 CC Arg696Pro amino acid substitution and disruption of a consensus Ser/Thr
 CC kinase phosphorylation site. The present sequence is a primer that can be
 CC used in a claimed method for detecting a disruptive mutation in the IKAP
 CC gene, using single-strand conformational polymorphism (SSCP) analysis.
 CC The primer was used in the genotype analysis of FD alleles. Use with the
 CC primer given in ABN84784 yielded a 244 bp fragment. In a family with
 CC probands heterozygous for the major haplotype, all affected individuals
 CC were homoallelic for 2507+6C to C and all the parents were heterozygous.
 CC In families with probands heterozygous for the major and minor 2 FD
 CC haplotypes, 1 parent and the proband were heterozygous for R696P and the
 CC other parent and the proband were heterozygous for 2507+6T to C. Analysis
 CC of 31 probands homozygous for the major FD haplotype showed that 100% of
 CC the probands were homozygous for 2507+6T to C, 100% of the parents were
 CC heterozygous for this mutation, and 4 siblings of the probands had FD and
 CC were homozygous for the FD haplotype and the 2507+6T to C mutation. Study
 CC of a random group of 619 individuals of Ashkenazi Jewish descent revealed
 CC the presence of 25 carriers of 2507+6T to C and 2 individuals with R696P.
 CC The method is useful for FD diagnosis and for identifying carriers of the
 CC condition
 XX
 XX SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTCGCAAAACAGTACATGG 20
 DB 1 AGTCGCAAAACAGTACATGG 20
 |||||
 |||||

RESULT 2

ABQ80567/c
 ID ABQ80567 standard; DNA; 66479 BP.

AC ABQ80567;
 XX

DT 08-NOV-2002 (first entry)
 XX

DE Mutant human IKKAP gene #2.
 XX

XX Human; IKKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
 XX PD2; mutation; gene; chromosome 9q31; ds.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

XX Key Location/Qualifiers
 XX mutation replace(33714,G)
 XX /*tag= a

XX WO200259381-A2.
 XX

XX 01-AUG-2002.
 XX

XX 07-JAN-2002; 2002WO-US000473.
 XX

XX 06-JAN-2001; 2001US-0260080P.
 XX

XX (GEO) GEN HOSPITAL CORP.
 XX